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09/765272

ATTACH TO  
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SEQUENCE LISTING

(1) GENERAL INFORMATION:

TECH CENTER 1600/2900

(i) APPLICANT: Choi et. al.

(ii) TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines

(iii) NUMBER OF SEQUENCES: 454

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Human Genome Sciences, Inc.
- (B) STREET: 9410 Key West Avenue
- (C) CITY: Rockville
- (D) STATE: Maryland
- (E) COUNTRY: USA
- (F) ZIP: 20850

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
- (B) COMPUTER: Dell Latitude C610
- (C) OPERATING SYSTEM: Windows 2000
- (D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/765,272
- (B) FILING DATE: January 22, 2001
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/961,083
- (B) FILING DATE: OCT-30-1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Lin J. Hymel
- (B) REGISTRATION NUMBER: 45,414
- (C) REFERENCE/DOCKET NUMBER: PB340P2C2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (301) 610-5790
- (B) TELEFAX: (301) 309-8439

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TAAAATCTAC GACAATAAAA ATCAACTCAT TGCTGACTTG GGTTCCTGAAC GCCGCGTCAA 60  
 TGCCCAAGCT AATGATATTC CCACAGATTT GGTAAAGGCA ATCGTTTCTA TCGAAGACCA 120  
 TCGCTTCTTC GACCACAGGG GGATTGATAC CATCCGTATC CTGGGAGCTT TCTTGCGCAA 180  
 TCTGCAAAGC AATTCCCTCC AAGGTGGATC AACTCTCACC CAACAGTTGA TTAAGTTGAC 240  
 TTACTTTTCA ACTTCGACTT CCGACCAGAC TATTTCTCGT AAGGCTCAGG AAGCTTGGTT 300  
 AGCGATTGAG TTAGAACAAA AAGCAACCAA GCAAGAAATC TTGACCTACT ATATAAATAA 360  
 GGTCTACATG TCTAATGGGA ACTATGGAAT GCAGACAGCA GCTCAAAACT ACTATGGTAA 420  
 AGACCTCAAT AATTTAAGTT TACCTCAGTT AGCCTTGCTG GCTGGAATGC CTCAGGCACC 480  
 AAACCAATAT GACCCCTATT CACATCCAGA AGCAGCCCAA GACCGCCGAA ACTTGGTCTT 540  
 ATCTGAAATG AAAAATCAAG GCTACATCTC TGCTGAACAG TATGAGAAAG CAGTCAATAC 600  
 ACCAATTACT GATGGACTAC AAAGTCTCAA ATCAGCAAGT AATTACCTTG CTTACATGGA 660  
 TAATTACCTC AAGGAAGTCA TCAATCAAGT TGAAGAAGAA ACAGGCTATA ACCTACTCAC 720  
 AACTGGGATG GATGTCTACA CAAATGTAGA CCAAGAAGCT CAAAAACATC TGTGGGATAT 780  
 TTACAATACA GACGAATACG TTGCCTATCC AGACGATGAA TTGCAAGTCG CTTCTACCAT 840  
 TGTTGATGTT TCTAACGGTA AAGTCATTGC CCAGCTAGGA GCACGCCATC AGTCAAGTAA 900  
 TGTTTCCTTC GGAATTAACC AAGCAGTAGA AACAAACCGC GACTGGGGAT CAACTATGAA 960  
 ACCGATCACA GACTATGCTC CTGCCTTGGA GTACGGTGTC TACGATTCAA CTGCTACTAT 1020  
 CGTTCACGAT GAGCCCTATA ACTACCCTGG GACAAATACT CCTGTTTATA ACTGGGATAG 1080  
 GGGCTACTTT GGCAACATCA CCTTGCAATA CGCCCTGCAA CAATCGCGAA ACGTCCCAGC 1140  
 CGTGGAACCT CTAAACAAGG TCGGACTCAA CCGCGCCAAG ACTTTCTTAA ATGGTCTAGG 1200  
 AATCGACTAC CCAAGTATTC ACTACTCAAA TGCCATTTCA AGTAACACAA CCGAATCAGA 1260  
 CAAAAAATAT GGAGCAAGTA GTGAAAAGAT GGCTGCTGCT TACGCTGCCT TTGCAAATGG 1320  
 TGGAACCTAC TATAAACCAA TGTATATCCA TAAAGTCGTC TTTAGTGATG GGAGTGAAAA 1380  
 AGAGTTCTCT AATGTCGGAA CTCGTGCCAT GAAGGAAACG ACAGCCTATA TGATGACCGA 1440  
 CATGATGAAA ACAGTCTTGA CTTATGGAAC TGGACGAAAT GCCTATCTTG CTTGGCTCCC 1500  
 TCAGGCTGGT AAAACAGGAA CCTCTAACTA TACAGACGAG GAAATTGAAA ACCACATCAA 1560  
 GACCTCTCAA TTTGTAGCAC CTGATGAACT ATTTGCTGGC TATACGCGTA AATATTCAAT 1620  
 GGCTGTATGG ACAGGCTATT CTAACCGTCT GACACCACCT GTAGGCAATG GCCTTACGGT 1680  
 CGCTGCCAAA GTTTACCGCT CTATGATGAC CTACCTGTCT GAAGGAAGCA ATCCAGAAGA 1740  
 TTGGAATATA CCAGAGGGGC TCTACAGAAA TGGAGAATTC GTATTTAAAA ATGGTGCTCG 1800

TTCTACGTGG AACTCACCTG CTCCACAACA ACCCCCATCA ACTGAAAGTT CAAGCTCATC 1860  
 ATCAGATAGT TCAACTTCAC AGTCTAGCTC AACCCTCCA AGCACAAATA ATAGTACGAC 1920  
 TACCAATCCT AACAATAATA CGCAACAATC AAATACAACC CCTGATCAAC AAAATCAGAA 1980  
 TCCTCAACCA GCACAACCA 1999

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Ile Tyr Asp Asn Lys Asn Gln Leu Ile Ala Asp Leu Gly Ser Glu  
 1 5 10 15  
 Arg Arg Val Asn Ala Gln Ala Asn Asp Ile Pro Thr Asp Leu Val Lys  
 20 25 30  
 Ala Ile Val Ser Ile Glu Asp His Arg Phe Phe Asp His Arg Gly Ile  
 35 40 45  
 Asp Thr Ile Arg Ile Leu Gly Ala Phe Leu Arg Asn Leu Gln Ser Asn  
 50 55 60  
 Ser Leu Gln Gly Gly Ser Thr Leu Thr Gln Gln Leu Ile Lys Leu Thr  
 65 70 75 80  
 Tyr Phe Ser Thr Ser Thr Ser Asp Gln Thr Ile Ser Arg Lys Ala Gln  
 85 90 95  
 Glu Ala Trp Leu Ala Ile Gln Leu Glu Gln Lys Ala Thr Lys Gln Glu  
 100 105 110  
 Ile Leu Thr Tyr Tyr Ile Asn Lys Val Tyr Met Ser Asn Gly Asn Tyr  
 115 120 125  
 Gly Met Gln Thr Ala Ala Gln Asn Tyr Tyr Gly Lys Asp Leu Asn Asn  
 130 135 140  
 Leu Ser Leu Pro Gln Leu Ala Leu Leu Ala Gly Met Pro Gln Ala Pro  
 145 150 155 160  
 Asn Gln Tyr Asp Pro Tyr Ser His Pro Glu Ala Ala Gln Asp Arg Arg  
 165 170 175  
 Asn Leu Val Leu Ser Glu Met Lys Asn Gln Gly Tyr Ile Ser Ala Glu  
 180 185 190  
 Gln Tyr Glu Lys Ala Val Asn Thr Pro Ile Thr Asp Gly Leu Gln Ser  
 195 200 205  
 Leu Lys Ser Ala Ser Asn Tyr Pro Ala Tyr Met Asp Asn Tyr Leu Lys  
 210 215 220  
 Glu Val Ile Asn Gln Val Glu Glu Glu Thr Gly Tyr Asn Leu Leu Thr



225					230					235				240	
Thr	Gly	Met	Asp	Val	Tyr	Thr	Asn	Val	Asp	Gln	Glu	Ala	Gln	Lys	His
				245					250					255	
Leu	Trp	Asp	Ile	Tyr	Asn	Thr	Asp	Glu	Tyr	Val	Ala	Tyr	Pro	Asp	Asp
			260					265					270		
Glu	Leu	Gln	Val	Ala	Ser	Thr	Ile	Val	Asp	Val	Ser	Asn	Gly	Lys	Val
		275					280					285			
Ile	Ala	Gln	Leu	Gly	Ala	Arg	His	Gln	Ser	Ser	Asn	Val	Ser	Phe	Gly
	290					295					300				
Ile	Asn	Gln	Ala	Val	Glu	Thr	Asn	Arg	Asp	Trp	Gly	Ser	Thr	Met	Lys
305					310					315					320
Pro	Ile	Thr	Asp	Tyr	Ala	Pro	Ala	Leu	Glu	Tyr	Gly	Val	Tyr	Asp	Ser
				325					330					335	
Thr	Ala	Thr	Ile	Val	His	Asp	Glu	Pro	Tyr	Asn	Tyr	Pro	Gly	Thr	Asn
			340					345					350		
Thr	Pro	Val	Tyr	Asn	Trp	Asp	Arg	Gly	Tyr	Phe	Gly	Asn	Ile	Thr	Leu
		355					360					365			
Gln	Tyr	Ala	Leu	Gln	Gln	Ser	Arg	Asn	Val	Pro	Ala	Val	Glu	Thr	Leu
	370					375					380				
Asn	Lys	Val	Gly	Leu	Asn	Arg	Ala	Lys	Thr	Phe	Leu	Asn	Gly	Leu	Gly
385					390					395					400
Ile	Asp	Tyr	Pro	Ser	Ile	His	Tyr	Ser	Asn	Ala	Ile	Ser	Ser	Asn	Thr
				405					410					415	
Thr	Glu	Ser	Asp	Lys	Lys	Tyr	Gly	Ala	Ser	Ser	Glu	Lys	Met	Ala	Ala
			420					425					430		
Ala	Tyr	Ala	Ala	Phe	Ala	Asn	Gly	Gly	Thr	Tyr	Tyr	Lys	Pro	Met	Tyr
		435					440					445			
Ile	His	Lys	Val	Val	Phe	Ser	Asp	Gly	Ser	Glu	Lys	Glu	Phe	Ser	Asn
	450					455					460				
Val	Gly	Thr	Arg	Ala	Met	Lys	Glu	Thr	Thr	Ala	Tyr	Met	Met	Thr	Asp
465					470					475					480
Met	Met	Lys	Thr	Val	Leu	Thr	Tyr	Gly	Thr	Gly	Arg	Asn	Ala	Tyr	Leu
				485					490					495	
Ala	Trp	Leu	Pro	Gln	Ala	Gly	Lys	Thr	Gly	Thr	Ser	Asn	Tyr	Thr	Asp
			500					505					510		
Glu	Glu	Ile	Glu	Asn	His	Ile	Lys	Thr	Ser	Gln	Phe	Val	Ala	Pro	Asp
		515					520					525			
Glu	Leu	Phe	Ala	Gly	Tyr	Thr	Arg	Lys	Tyr	Ser	Met	Ala	Val	Trp	Thr
	530					535					540				
Gly	Tyr	Ser	Asn	Arg	Leu	Thr	Pro	Leu	Val	Gly	Asn	Gly	Leu	Thr	Val
545					550					555					560
Ala	Ala	Lys	Val	Tyr	Arg	Ser	Met	Met	Thr	Tyr	Leu	Ser	Glu	Gly	Ser
				565					570					575	

Asn Pro Glu Asp Trp Asn Ile Pro Glu Gly Leu Tyr Arg Asn Gly Glu  
 580 585 590  
 Phe Val Phe Lys Asn Gly Ala Arg Ser Thr Trp Asn Ser Pro Ala Pro  
 595 600 605  
 Gln Gln Pro Pro Ser Thr Glu Ser Ser Ser Ser Ser Ser Asp Ser Ser  
 610 615 620  
 Thr Ser Gln Ser Ser Ser Thr Thr Pro Ser Thr Asn Asn Ser Thr Thr  
 625 630 635 640  
 Thr Asn Pro Asn Asn Asn Thr Gln Gln Ser Asn Thr Thr Pro Asp Gln  
 645 650 655  
 Gln Asn Gln Asn Pro Gln Pro Ala Gln Pro  
 660 665

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAATTACAAT ACGGACTATG AATTGACCTC TGGAGAAAAA TTACCTCTTC CTAAAGAGAT 60  
 TTCAGGTTAC ACTTATATTG GATATATCAA AGAGGGAAAA ACGACTTCTG AGTCTGAAGT 120  
 AAGTAATCAA AAGAGTTCAG TTGCCACTCC TACAAAACAA CAAAAGGTGG ATTATAATGT 180  
 TACACCGAAT TTTGTAGACC ATCCATCAAC AGTACAAGCT ATTCAGGAAC AAACACCTGT 240  
 TTCTTCAACT AAGCCGACAG AAGTTCAAGT AGTTGAAAAA CCTTCTCTTA CTGAATTAAT 300  
 CAATCCAAGA AAAGAAGAGA AACAATCTTC AGATTCTCAA GAACAATTAG CCGAACATAA 360  
 GAATCTAGAA ACGAAGAAAG AGGAGAAGAT TTCTCCAAAA GAAAAGACTG GGGTAAATAC 420  
 ATTAAATCCA CAGGATGAAG TTTTATCAGG TCAATTGAAC AAACCTGAAC TCTTATATCG 480  
 TGAGGAAACT ATGGAGACAA AAATAGATTT TCAAGAAGAA ATTCAAGAAA ATCCTGATTT 540  
 AGCTGAAGGA ACTGTAAGAG TAAAACAAGA AGGTAAATTA GGTAAGAAAG TTGAAATCGT 600  
 CAGAATATTC TCTGTAAACA AGGAAGAAGT TTCGCGAGAA ATTGTTTCAA CTTCAACGAC 660  
 TGCGCCTAGT CCAAGAATAG TCGAAAAAGG TACTAAAAAA ACTCAAGTTA TAAAGGAACA 720  
 ACCTGAGACT GGTGTAGAAC ATAAGGACGT ACAGTCTGGA GCTATTGTTG AACCCGCAAT 780  
 TCAGCCTGAG TTGCCCCGAAG CTGTAGTAAG TGACAAAGGC GAACCAGAAG TTCAACCTAC 840  
 ATTACCCGAA GCAGTTGTGA CCGACAAAGG TGAGACTGAG GTTCAACCAG AGTCGCCAGA 900  
 TACTGTGGTA AGTGATAAAG GTGAACCAGA GCAGGTAGCA CCGCTTCCAG AATATAAGGG 960  
 TAATATTGAG CAAGTAAAC CTGAAACTCC GGTGAGAAG ACCAAAGAAC AAGGTCCAGA 1020

AAAAACTGAA GAAGTTCCAG TAAAACCAAC AGAAGAAACA CCAGTAAATC CAAATGAAGG	1080
TACTACAGAA GGAACCTCAA TTCAAGAAGC AGAAAATCCA GTTCAACCTG CAGAAGAATC	1140
AACAACGAAT TCAGAGAAAG TATCACCAGA TACATCTAGC AAAAATACTG GGGAAGTGTC	1200
CAGTAATCCT AGTGATTCTGA CAACCTCAGT TGGAGAATCA AATAAACCCAG AACATAATGA	1260
CTCTAAAAAT GAAAATTCAG AAAAACTGT AGAAGAAGTT CCAGTAAATC CAAATGAAGG	1320
CACAGTAGAA GGTACCTCAA ATCAAGAAAC AGAAAAACCA GTTCAACCTG CAGAAGAAAC	1380
ACAAACAAAC TCTGGGAAAA TAGCTAACGA AAATACTGGA GAAGTATCCA ATAAACCTAG	1440
TGATTCAAAA CCACCAGTTG AAGAATCAAA TCAACCAGAA AAAAACGGAA CTGCAACAAA	1500
ACCAGAAAAT TCAGGTAATA CAACATCAGA GAATGGACAA ACAGAACCAG AACCATCAAA	1560
CGGAAATTCA ACTGAGGATG TTTCAACCGA ATCAAACACA TCCAATTCAA ATGGAAACGA	1620
AGAAATTAAA CAAGAAAATG AACTAGACCC TGATAAAAAG GTAGAAGAAC CAGAGAAAAC	1680
ACTTGAATTA AGAAATGTTT CCGACCTAGA GTTA	1714


## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:



Asn	Tyr	Asn	Thr	Asp	Tyr	Glu	Leu	Thr	Ser	Gly	Glu	Lys	Leu	Pro	Leu
1				5					10					15	
Pro	Lys	Glu	Ile	Ser	Gly	Tyr	Thr	Tyr	Ile	Gly	Tyr	Ile	Lys	Glu	Gly
			20					25					30		
Lys	Thr	Thr	Ser	Glu	Ser	Glu	Val	Ser	Asn	Gln	Lys	Ser	Ser	Val	Ala
			35				40					45			
Thr	Pro	Thr	Lys	Gln	Gln	Lys	Val	Asp	Tyr	Asn	Val	Thr	Pro	Asn	Phe
			50			55					60				
Val	Asp	His	Pro	Ser	Thr	Val	Gln	Ala	Ile	Gln	Glu	Gln	Thr	Pro	Val
					70					75				80	
Ser	Ser	Thr	Lys	Pro	Thr	Glu	Val	Gln	Val	Val	Glu	Lys	Pro	Phe	Ser
				85					90					95	
Thr	Glu	Leu	Ile	Asn	Pro	Arg	Lys	Glu	Glu	Lys	Gln	Ser	Ser	Asp	Ser
			100					105					110		
Gln	Glu	Gln	Leu	Ala	Glu	His	Lys	Asn	Leu	Glu	Thr	Lys	Lys	Glu	Glu
			115				120					125			
Lys	Ile	Ser	Pro	Lys	Glu	Lys	Thr	Gly	Val	Asn	Thr	Leu	Asn	Pro	Gln
						135					140				

Asp Glu Val Leu Ser Gly Gln Leu Asn Lys Pro Glu Leu Leu Tyr Arg  
 145 150 155 160  
 Glu Glu Thr Met Glu Thr Lys Ile Asp Phe Gln Glu Glu Ile Gln Glu  
 165 170 175  
 Asn Pro Asp Leu Ala Glu Gly Thr Val Arg Val Lys Gln Glu Gly Lys  
 180 185 190  
 Leu Gly Lys Lys Val Glu Ile Val Arg Ile Phe Ser Val Asn Lys Glu  
 195 200 205  
 Glu Val Ser Arg Glu Ile Val Ser Thr Ser Thr Thr Ala Pro Ser Pro  
 210 215 220  
 Arg Ile Val Glu Lys Gly Thr Lys Lys Thr Gln Val Ile Lys Glu Gln  
 225 230 235 240  
 Pro Glu Thr Gly Val Glu His Lys Asp Val Gln Ser Gly Ala Ile Val  
 245 250 255  
 Glu Pro Ala Ile Gln Pro Glu Leu Pro Glu Ala Val Val Ser Asp Lys  
 260 265 270  
 Gly Glu Pro Glu Val Gln Pro Thr Leu Pro Glu Ala Val Val Thr Asp  
 275 280 285  
 Lys Gly Glu Thr Glu Val Gln Pro Glu Ser Pro Asp Thr Val Val Ser  
 290 295 300  
 Asp Lys Gly Glu Pro Glu Gln Val Ala Pro Leu Pro Glu Tyr Lys Gly  
 305 310 315 320  
 Asn Ile Glu Gln Val Lys Pro Glu Thr Pro Val Glu Lys Thr Lys Glu  
 325 330 335  
 Gln Gly Pro Glu Lys Thr Glu Glu Val Pro Val Lys Pro Thr Glu Glu  
 340 345 350  
 Thr Pro Val Asn Pro Asn Glu Gly Thr Thr Glu Gly Thr Ser Ile Gln  
 355 360 365  
 Glu Ala Glu Asn Pro Val Gln Pro Ala Glu Glu Ser Thr Thr Asn Ser  
 370 375 380  
 Glu Lys Val Ser Pro Asp Thr Ser Ser Lys Asn Thr Gly Glu Val Ser  
 385 390 395 400  
 Ser Asn Pro Ser Asp Ser Thr Thr Ser Val Gly Glu Ser Asn Lys Pro  
 405 410 415  
 Glu His Asn Asp Ser Lys Asn Glu Asn Ser Glu Lys Thr Val Glu Glu  
 420 425 430  
 Val Pro Val Asn Pro Asn Glu Gly Thr Val Glu Gly Thr Ser Asn Gln  
 435 440 445  
 Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn Ser  
 450 455 460  
 Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro Ser  
 465 470 475 480

Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn Gly  
 485 490 495  
 Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn Gly  
 500 505 510  
 Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val Ser  
 515 520 525  
 Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys Gln  
 530 535 540  
 Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys Thr  
 545 550 555 560  
 Leu Glu Leu Arg Asn Val Ser Asp Leu Glu Leu  
 565 570

## (2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 748 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGAGAATCAA GCTACACCCA AAGAGACTAG CGCTCAAAAG ACAATCGTCC TTGCTACAGC 60  
 TGGCGACGTG CCACCATTGT ACTACGAAGA CAAGGGCAAT CTGACAGGCT TTGATATCGA 120  
 AGTTTTAAAG GCAGTAGATG AAAAATCAG CGACTACGAG ATTCAATTCC AAAGAACCGC 180  
 CTGGGAGAGC ATCTTCCAG GACTTGATTC TGGTCACTAT CAGGCTGCGG CCAATAACTT 240  
 GAGTTACACA AAAGAGCGTG CTGAAAAATA CCTTTACTCG CTTCCAATTT CCAACAATCC 300  
 CCTCGTCCTT GTCAGCAACA AGAAAAATCC TTTGACTTCT CTTGACCAGA TCGCTGGTAA 360  
 AACAAACACAA GAGGATACCG GAACCTCTAA CGCTCAATTC ATCAATAACT GGAATCAGAA 420  
 ACACACTGAT AATCCCGCTA CAATTAATTT TTCTGGTGAG GATATTGGTA AACGAATCCT 480  
 AGACCTTGCT AACGGAGAGT TTGATTTCTT AGTTTTTGAC AAGGTATCCG TTCAAAAGAT 540  
 TATCAAGGAC CGTGGTTTAG ACCTCTCAGT CGTTGATTTA CCTTCTGCAG ATAGCCCCAG 600  
 CAATTATATC ATTTTCTCAA GCGACCAAAA AGAGTTTAAA GAGCAATTTG ATAAAGCGCT 660  
 CAAAGAACTC TATCAAGACG GAACCCTTGA AAAACTCAGC AATACCTATC TAGGTGGTTC 720  
 TTACCTCCCA GATCAATCTC AGTTACAA 748

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 249 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Asn Gln Ala Thr Pro Lys Glu Thr Ser Ala Gln Lys Thr Ile Val  
1 5 10 15  
Leu Ala Thr Ala Gly Asp Val Pro Pro Phe Asp Tyr Glu Asp Lys Gly  
20 25 30  
Asn Leu Thr Gly Phe Asp Ile Glu Val Leu Lys Ala Val Asp Glu Lys  
35 40 45  
Leu Ser Asp Tyr Glu Ile Gln Phe Gln Arg Thr Ala Trp Glu Ser Ile  
50 55 60  
Phe Pro Gly Leu Asp Ser Gly His Tyr Gln Ala Ala Ala Asn Asn Leu  
65 70 75 80  
Ser Tyr Thr Lys Glu Arg Ala Glu Lys Tyr Leu Tyr Ser Leu Pro Ile  
85 90 95  
Ser Asn Asn Pro Leu Val Leu Val Ser Asn Lys Lys Asn Pro Leu Thr  
100 105 110  
Ser Leu Asp Gln Ile Ala Gly Lys Thr Thr Gln Glu Asp Thr Gly Thr  
115 120 125  
Ser Asn Ala Gln Phe Ile Asn Asn Trp Asn Gln Lys His Thr Asp Asn  
130 135 140  
Pro Ala Thr Ile Asn Phe Ser Gly Glu Asp Ile Gly Lys Arg Ile Leu  
145 150 155 160  
Asp Leu Ala Asn Gly Glu Phe Asp Phe Leu Val Phe Asp Lys Val Ser  
165 170 175  
Val Gln Lys Ile Ile Lys Asp Arg Gly Leu Asp Leu Ser Val Val Asp  
180 185 190  
Leu Pro Ser Ala Asp Ser Pro Ser Asn Tyr Ile Ile Phe Ser Ser Asp  
195 200 205  
Gln Lys Glu Phe Lys Glu Gln Phe Asp Lys Ala Leu Lys Glu Leu Tyr  
210 215 220  
Gln Asp Gly Thr Leu Glu Lys Leu Ser Asn Thr Tyr Leu Gly Gly Ser  
225 230 235 240  
Tyr Leu Pro Asp Gln Ser Gln Leu Gln  
245

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 985 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGGTAACCGC TCTTCTCGTA ACGCAGCTTC ATCTTCTGAT GTGAAGACAA AAGCAGCAAT 60  
 CGTCACTGAT ACTGGTGGTG TTGATGACAA ATCATTCAAC CAATCAGCTT GGGAAGGTTT 120  
 GCAGGCTTGG GGTAAGAAGC ACAATCTTTC AAAAGATAAC GGTTCCTACTT ACTTCCAATC 180  
 AACAAAGTGA GCTGACTACG CTAACAACCTT GCAACAAGCG GCTGGAAGTT ACAACCTAAT 240  
 CTTCCGGTGT GGTTTTGCCC TTAATAATGC AGTTAAAGAT GCAGCAAAAAG AACACACTGA 300  
 CTTGAACTAT GTCTTGATTG ATGATGTGAT TAAAGACCAA AAGAATGTTG CGAGCGTAAC 360  
 TTTCCGTGAT AATGAGTCAG GTTACCTTGC AGGTGTGGCT GCAGCAAAAA CAACTAAGAC 420  
 AAAACAAGTT GGTTTTGTAG GTGGTATCGA ATCTGAAGTT ATCTCTCGTT TTGAAGCAGG 480  
 ATTCAAGGCT GGTGTTGCGT CAGTAGACCC ATCTATCAAA GTCCAAGTTG ACTACGCTGG 540  
 TTCATTTGGT GATGCGGCTA AAGGTAAAAC AATTGCAGCC GCACAATACG CAGCCGGTGC 600  
 AGATATTGTT TACCAAGTAG CTGGTGGTAC AGGTGCAGGT GTCTTTGCAG AGGCAAAATC 660  
 TCTCAACGAA AGCCGTCCTG AAAATGAAAA AGTTTGGGTT ATCGGTGTTG ATCGTGACCA 720  
 AGAAGCAGAA GGTAATACA CTTCTAAAGA TGGCAAAGAA TCAAACTTTG TTCTTGATC 780  
 TACTTTGAAA CAAGTTGGTA CAACTGTAAA AGATATTTCT AACAAGGCAG AAAGAGGAGA 840  
 ATTCCCTGGC GGTCAAGTGA TCGTTTACTC ATTGAAGGAT AAAGGGGTTG ACTTGGCAGT 900  
 AACAAACCTT TCAGAAGAAG GTAAAAAAGC TGTCGAAGAT GCAAAAGCTA AAATCCTTGA 960  
 TGGAAGCGTA AAAGTTCCTG AAAAA 985

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Asn Arg Ser Ser Arg Asn Ala Ala Ser Ser Ser Asp Val Lys Thr  
 1 5 10 15  
 Lys Ala Ala Ile Val Thr Asp Thr Gly Gly Val Asp Asp Lys Ser Phe  
 20 25 30  
 Asn Gln Ser Ala Trp Glu Gly Leu Gln Ala Trp Gly Lys Glu His Asn  
 35 40 45  
 Leu Ser Lys Asp Asn Gly Phe Thr Tyr Phe Gln Ser Thr Ser Glu Ala  
 50 55 60  
 Asp Tyr Ala Asn Asn Leu Gln Gln Ala Ala Gly Ser Tyr Asn Leu Ile  
 65 70 75 80  
 Phe Gly Val Gly Phe Ala Leu Asn Asn Ala Val Lys Asp Ala Ala Lys  
 85 90 95

Glu His Thr Asp Leu Asn Tyr Val Leu Ile Asp Asp Val Ile Lys Asp  
 100 105 110  
 Gln Lys Asn Val Ala Ser Val Thr Phe Ala Asp Asn Glu Ser Gly Tyr  
 115 120 125  
 Leu Ala Gly Val Ala Ala Ala Lys Thr Thr Lys Thr Lys Gln Val Gly  
 130 135 140  
 Phe Val Gly Gly Ile Glu Ser Glu Val Ile Ser Arg Phe Glu Ala Gly  
 145 150 155 160  
 Phe Lys Ala Gly Val Ala Ser Val Asp Pro Ser Ile Lys Val Gln Val  
 165 170 175  
 Asp Tyr Ala Gly Ser Phe Gly Asp Ala Ala Lys Gly Lys Thr Ile Ala  
 180 185 190  
 Ala Ala Gln Tyr Ala Ala Gly Ala Asp Ile Val Tyr Gln Val Ala Gly  
 195 200 205  
 Gly Thr Gly Ala Gly Val Phe Ala Glu Ala Lys Ser Leu Asn Glu Ser  
 210 215 220  
 Arg Pro Glu Asn Glu Lys Val Trp Val Ile Gly Val Asp Arg Asp Gln  
 225 230 235 240  
 Glu Ala Glu Gly Lys Tyr Thr Ser Lys Asp Gly Lys Glu Ser Asn Phe  
 245 250 255  
 Val Leu Val Ser Thr Leu Lys Gln Val Gly Thr Thr Val Lys Asp Ile  
 260 265 270  
 Ser Asn Lys Ala Glu Arg Gly Glu Phe Pro Gly Gly Gln Val Ile Val  
 275 280 285  
 Tyr Ser Leu Lys Asp Lys Gly Val Asp Leu Ala Val Thr Asn Leu Ser  
 290 295 300  
 Glu Glu Gly Lys Lys Ala Val Glu Asp Ala Lys Ala Lys Ile Leu Asp  
 305 310 315 320  
 Gly Ser Val Lys Val Pro Glu Lys  
 325

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGTGGAAATT TGACAGGTAA CAGCAAAAAA GCTGCTGATT CAGGTGACAA ACCTGTTATC	60
AAAATGTACC AAATCGGTGA CAAACCAGAC AACTTGGATG AATTGTTAGC AAATGCCAAC	120
AAAATCATTG AAGAAAAAGT TGGTGCCAAA TTGGATATCC AATACCTTGG CTGGGGTGAC	180
TATGGTAAGA AAATGTCAGT TATCACATCA TCTGGTGAAA ACTATGATAT TGCCTTTGCA	240





GATAACTATA TTGTAAATGC TCAAAAAGGT GCTTACGCTG ACTTGACAGA ATTGTACAAA	300
AAAGAAGGTA AAGACCTTTA CAAAGCAC TT GACCCAGCTT ACATCAAGGG TAATACTGTA	360
AATGGTAAGA TTTACGCTGT TCCAGTTGCA GCCAACGTTG CATCATCTCA AAAC TTTGCC	420
TTCAACGGAA CTCTCCTTGC TAAATATGGT ATCGATATTT CAGGTGTTAC TTCTTACGAA	480
ACTCTTGAGC CAGTCTTGAA ACAAATCAAA GAAAAAGCTC CAGACGTAGT ACCATTTGCT	540
ATTGGTAAAG TTTTCATCCC ATCTGATAAT TTTGACTACC CAGTAGCAAA CGGTCTTCCA	600
TTCGTTATCG ACCTTGAAGG CGATACTACT AAAGTTGTAA ACCGTTACGA AGTGCCCTCGT	660
TTCAAAGAAC ACTTGAAGAC TCTTCACAAA TTCTATGAAG CTGGCTACAT TCCAAAAGAC	720
GTCGCAACAA GCGATACTTC CTTTGACCTT CAACAAGATA CTTGGTTCGT TCGTGAAGAA	780
ACAGTAGGAC CAGCTGACTA CGGTAACAGC TTGCTTTTCAC GTGTTGCCAA CAAAGATATC	840
CAAATCAAAC CAATTACTAA CTTTCATCAAG NAAAACCAAA CAACACAAGT TGC'TAACTTT	900
GTCATCTCAA ACAACTCTAA GAACAAAGAA AAATCAATGG AAATCTTGAA CCTCTTGAAT	960
ACGAACCCAG AACTCTTGAA CGGTCTTGTT TACGGTCCAG AAGGCAAGAA CTGGGAAAAA	1020
ATTGAAGGTA AAGAAAACCG TGTTCGCGTT CTTGATGGCT ACAAAGGAAA CACTCACATG	1080
GGTGGATGGA ACACTGGTAA CAACTGGATC CTTTACATCA ACGAAAACGT TACAGACCAA	1140
CAAATCGAAA ATTCTAAGAA AGAATTGGCA GAAGCTAAAG AATCTCCAGC GCTTGGATTT	1200
ATCTTCAATA CTGACAATGT GAAATCTGAA ATCTCAGCTA TTGCTAACAC AATGCAACAA	1260
TTTGATACAG CTATCAACAC TGGTACTGTA GACCCAGATA AAGCGATTCC AGAATTGATG	1320
GAAAAATTGA AATCTGAAGG TGCCTACGAA AAAGTATTGA ACGAAATGCA AAAACAATAC	1380
GATGAATTCT TGAAAAACAA AAAA	1404

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys	Gly	Asn	Leu	Thr	Gly	Asn	Ser	Lys	Lys	Ala	Ala	Asp	Ser	Gly	Asp
1				5				10						15	
Lys	Pro	Val	Ile	Lys	Met	Tyr	Gln	Ile	Gly	Asp	Lys	Pro	Asp	Asn	Leu
			20				25						30		
Asp	Glu	Leu	Leu	Ala	Asn	Ala	Asn	Lys	Ile	Ile	Glu	Glu	Lys	Val	Gly
		35				40					45				
Ala	Lys	Leu	Asp	Ile	Gln	Tyr	Leu	Gly	Trp	Gly	Asp	Tyr	Gly	Lys	Lys

50					55					60					
Met 65	Ser	Val	Ile	Thr	Ser 70	Ser	Gly	Glu	Asn	Tyr 75	Asp	Ile	Ala	Phe	Ala 80
Asp	Asn	Tyr	Ile	Val 85	Asn	Ala	Gln	Lys	Gly 90	Ala	Tyr	Ala	Asp	Leu	Thr 95
Glu	Leu	Tyr	Lys 100	Lys	Glu	Gly	Lys	Asp 105	Leu	Tyr	Lys	Ala	Leu	Asp	Pro 110
Ala	Tyr	Ile 115	Lys	Gly	Asn	Thr	Val 120	Asn	Gly	Lys	Ile	Tyr 125	Ala	Val	Pro
Val 130	Ala	Ala	Asn	Val	Ala	Ser 135	Ser	Gln	Asn	Phe	Ala 140	Phe	Asn	Gly	Thr
Leu 145	Leu	Ala	Lys	Tyr	Gly 150	Ile	Asp	Ile	Ser	Gly 155	Val	Thr	Ser	Tyr	Glu 160
Thr	Leu	Glu	Pro	Val 165	Leu	Lys	Gln	Ile	Lys 170	Glu	Lys	Ala	Pro	Asp	Val 175
Val	Pro	Phe	Ala 180	Ile	Gly	Lys	Val	Phe 185	Ile	Pro	Ser	Asp	Asn	Phe	Asp 190
Tyr	Pro	Val 195	Ala	Asn	Gly	Leu	Pro 200	Phe	Val	Ile	Asp	Leu 205	Glu	Gly	Asp
Thr 210	Thr	Lys	Val	Val	Asn	Arg 215	Tyr	Glu	Val	Pro	Arg 220	Phe	Lys	Glu	His
Leu 225	Lys	Thr	Leu	His	Lys 230	Phe	Tyr	Glu	Ala	Gly 235	Tyr	Ile	Pro	Lys	Asp 240
Val	Ala	Thr	Ser	Asp 245	Thr	Ser	Phe	Asp	Leu 250	Gln	Gln	Asp	Thr	Trp	Phe 255
Val	Arg	Glu	Glu 260	Thr	Val	Gly	Pro 265	Ala	Asp	Tyr	Gly	Asn	Ser 270	Leu	Leu
Ser	Arg	Val 275	Ala	Asn	Lys	Asp	Ile 280	Gln	Ile	Lys	Pro	Ile 285	Thr	Asn	Phe
Ile 290	Lys	Xaa	Asn	Gln	Thr	Thr 295	Gln	Val	Ala	Asn	Phe 300	Val	Ile	Ser	Asn
Asn 305	Ser	Lys	Asn	Lys	Glu 310	Lys	Ser	Met	Glu	Ile 315	Leu	Asn	Leu	Leu	Asn 320
Thr	Asn	Pro	Glu	Leu 325	Leu	Asn	Gly	Leu	Val 330	Tyr	Gly	Pro	Glu	Gly	Lys 335
Asn	Trp	Glu	Lys 340	Ile	Glu	Gly	Lys	Glu 345	Asn	Arg	Val	Arg	Val 350	Leu	Asp
Gly	Tyr	Lys 355	Gly	Asn	Thr	His	Met 360	Gly	Gly	Trp	Asn	Thr 365	Gly	Asn	Asn
Trp	Ile 370	Leu	Tyr	Ile	Asn	Glu 375	Asn	Val	Thr	Asp	Gln 380	Gln	Ile	Glu	Asn
Ser 385	Lys	Lys	Glu	Leu	Ala 390	Glu	Ala	Lys	Glu	Ser 395	Pro	Ala	Leu	Gly	Phe 400

Ile Phe Asn Thr Asp Asn Val Lys Ser Glu Ile Ser Ala Ile Ala Asn  
 405 410 415  
 Thr Met Gln Gln Phe Asp Thr Ala Ile Asn Thr Gly Thr Val Asp Pro  
 420 425 430  
 Asp Lys Ala Ile Pro Glu Leu Met Glu Lys Leu Lys Ser Glu Gly Ala  
 435 440 445  
 Tyr Glu Lys Val Leu Asn Glu Met Gln Lys Gln Tyr Asp Glu Phe Leu  
 450 455 460  
 Lys Asn Lys Lys  
 465

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGGTCAAGGA ACTGCTTCTA AAGACAACAA AGAGGCAGAA CTTAAGAAGG TTGACTTTAT 60  
 CCTAGACTGG ACACCAAATA CCAACCACAC AGGGCTTTAT GTTGCCAAGG AAAAAGGTTA 120  
 TTTCAAAGAA GCTGGAGTGG ATGTTGATTT GAAATTGCCA CCAGAAGAAA GTTCTTCTGA 180  
 CTTGGTTATC AACGGAAAGG CACCATTTCG AGTGTATTTT CAAGACTACA TGGCTAAGAA 240  
 ATTGGAAAAA GGAGCAGGAA TCACTGCCGT TGCAGCTATT GTTGAACACA ATACATCAGG 300  
 AATCATCTCT CGTAAATCTG ATAATGTAAG CAGTCCAAAA GACTTGGTTG GTAAGAAATA 360  
 TGGGACATGG AATGACCCAA CTGAACTTGC TATGTTGAAA ACCTTGGTAG AATCTCAAGG 420  
 TGGAGACTTT GAGAAGGTTG AAAAAGTACC AAATAACGAC TCAAAC TCAA TCACACCGAT 480  
 TGCCAATGGC GTCTTTGATA CTGCTTGGAT TTACTACGGT TGGGATGGTA TCCTTGCTAA 540  
 ATCTCAAGGT GTAGATGCTA ACTTCATGTA CTTGAAAGAC TATGTCAAGG AGTTTGACTA 600  
 CTATTCACCA GTTATCATCG CAAACAACGA CTATCTGAAA GATAACAAAG AAGAAGCTCG 660  
 CAAAGTCATC CAAGCCATCA AAAAAGGCTA CCAATATGCC ATGGAACATC CAGAAGAAGC 720  
 TGCAGATATT CTCATCAAGA ATGCACCTGA ACTCAAGGAA AACCGTGACT TTGTCATCGA 780  
 ATCTCAAAAA TACTTGTCAA AAGAATACGC AAGCGACAAG GAAAAATGGG GTCAATTTGA 840  
 CGCAGCTCGC TGGAATGCTT TCTACAAATG GGATAAAGAA AATGGTATCC TTAAAGAAGA 900  
 CTTGACAGAC AAAGGCTTCA CCAACGAATT TGTGAAA 937

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:


- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:



Gly	Gln	Gly	Thr	Ala	Ser	Lys	Asp	Asn	Lys	Glu	Ala	Glu	Leu	Lys	Lys
1				5					10					15	
Val	Asp	Phe	Ile	Leu	Asp	Trp	Thr	Pro	Asn	Thr	Asn	His	Thr	Gly	Leu
			20					25					30		
Tyr	Val	Ala	Lys	Glu	Lys	Gly	Tyr	Phe	Lys	Glu	Ala	Gly	Val	Asp	Val
		35					40					45			
Asp	Leu	Lys	Leu	Pro	Pro	Glu	Glu	Ser	Ser	Ser	Asp	Leu	Val	Ile	Asn
	50					55					60				
Gly	Lys	Ala	Pro	Phe	Ala	Val	Tyr	Phe	Gln	Asp	Tyr	Met	Ala	Lys	Lys
65					70					75					80
Leu	Glu	Lys	Gly	Ala	Gly	Ile	Thr	Ala	Val	Ala	Ala	Ile	Val	Glu	His
				85					90					95	
Asn	Thr	Ser	Gly	Ile	Ile	Ser	Arg	Lys	Ser	Asp	Asn	Val	Ser	Ser	Pro
			100					105					110		
Lys	Asp	Leu	Val	Gly	Lys	Lys	Tyr	Gly	Thr	Trp	Asn	Asp	Pro	Thr	Glu
		115					120					125			
Leu	Ala	Met	Leu	Lys	Thr	Leu	Val	Glu	Ser	Gln	Gly	Gly	Asp	Phe	Glu
	130					135					140				
Lys	Val	Glu	Lys	Val	Pro	Asn	Asn	Asp	Ser	Asn	Ser	Ile	Thr	Pro	Ile
145					150					155					160
Ala	Asn	Gly	Val	Phe	Asp	Thr	Ala	Trp	Ile	Tyr	Tyr	Gly	Trp	Asp	Gly
				165					170					175	
Ile	Leu	Ala	Lys	Ser	Gln	Gly	Val	Asp	Ala	Asn	Phe	Met	Tyr	Leu	Lys
			180					185					190		
Asp	Tyr	Val	Lys	Glu	Phe	Asp	Tyr	Tyr	Ser	Pro	Val	Ile	Ile	Ala	Asn
		195					200					205			
Asn	Asp	Tyr	Leu	Lys	Asp	Asn	Lys	Glu	Glu	Ala	Arg	Lys	Val	Ile	Gln
	210					215					220				
Ala	Ile	Lys	Lys	Gly	Tyr	Gln	Tyr	Ala	Met	Glu	His	Pro	Glu	Glu	Ala
225					230					235					240
Ala	Asp	Ile	Leu	Ile	Lys	Asn	Ala	Pro	Glu	Leu	Lys	Glu	Lys	Arg	Asp
				245					250					255	
Phe	Val	Ile	Glu	Ser	Gln	Lys	Tyr	Leu	Ser	Lys	Glu	Tyr	Ala	Ser	Asp
			260					265					270		
Lys	Glu	Lys	Trp	Gly	Gln	Phe	Asp	Ala	Ala	Arg	Trp	Asn	Ala	Phe	Tyr
		275					280					285			
Lys	Trp	Asp	Lys	Glu	Asn	Gly	Ile	Leu	Lys	Glu	Asp	Leu	Thr	Asp	Lys
	290					295					300				

Gly Phe Thr Asn Glu Phe Val Lys  
305 310

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TAGCTCAGGT GGAAACGCTG GTTCATCCTC TGGAAAAACA ACTGCCAAAG CTCGCACTAT 60  
CGATGAAATC AAAAAAAGCG GTGAACTGCG AATCGCCGTG TTTGGAGATA AAAAACCGTT 120  
TGGCTACGTT GACAATGATG GTTCTACCAA GGTACGCTAC GATATTGAAC TAGGGAACCA 180  
ACTAGCTCAA GACCTTGGTG TCAAGGTTAA ATACATTTCA GTCGATGCTG CCAACCGTGC 240  
GGAATACTTG ATTTCAAACA AGGTAGATAT TACTCTTGCT AACTTTACAG TAACTGACGA 300  
ACGTAAGAAA CAAGTTGATT TTGCCCTTCC ATATATGAAA GTTTCTCTGG GTGTCGTATC 360  
ACCTAAGACT GGTCTCATTA CAGACGTCAA ACAACTTGAA GTTAAACCT TAATTGTCAC 420  
AAAAGGAACG ACTGCTGAGA CTTATTTTGA AAAGAATCAT CCAGAAATCA AACTCCAAAA 480  
ATACGACCAA TACAGTGACT CTTACCAAGC TCTTCTTGAC GGACGTGGAG ATGCCTTTTTC 540  
AACTGACAAT ACGGAAGTTC TAGCTTGGGC GCTTGAAAAT AAAGGATTTG AAGTAGGAAT 600  
TACTTCCCTC GGTGATCCCG ATACCATTGC GGCAGCAGTT CAAAAAGGCA ACCAAGAATT 660  
GCTAGACTTC ATCAATAAAG ATATTGAAAA ATTAGGCAAG GAAAACCTTCT TCCACAAGGC 720  
CTATGAAAAG ACACCTCACC CAACCTACGG TGACGCTGCT AAAGCAGATG ACCTGGTTGT 780  
TGAAGGTGGA AAAGTTGAT 799

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Ser Gly Gly Asn Ala Gly Ser Ser Ser Gly Lys Thr Thr Ala Lys  
1 5 10 15  
Ala Arg Thr Ile Asp Glu Ile Lys Lys Ser Gly Glu Leu Arg Ile Ala  
20 25 30  
Val Phe Gly Asp Lys Lys Pro Phe Gly Tyr Val Asp Asn Asp Gly Ser  
35 40 45

Thr Lys Val Arg Tyr Asp Ile Glu Leu Gly Asn Gln Leu Ala Gln Asp  
 50 55 60  
 Leu Gly Val Lys Val Lys Tyr Ile Ser Val Asp Ala Ala Asn Arg Ala  
 65 70 75 80  
 Glu Tyr Leu Ile Ser Asn Lys Val Asp Ile Thr Leu Ala Asn Phe Thr  
 85 90 95  
 Val Thr Asp Glu Arg Lys Lys Gln Val Asp Phe Ala Leu Pro Tyr Met  
 100 105 110  
 Lys Val Ser Leu Gly Val Val Ser Pro Lys Thr Gly Leu Ile Thr Asp  
 115 120 125  
 Val Lys Gln Leu Glu Gly Lys Thr Leu Ile Val Thr Lys Gly Thr Thr  
 130 135 140  
 Ala Glu Thr Tyr Phe Glu Lys Asn His Pro Glu Ile Lys Leu Gln Lys  
 145 150 155 160  
 Tyr Asp Gln Tyr Ser Asp Ser Tyr Gln Ala Leu Leu Asp Gly Arg Gly  
 165 170 175  
 Asp Ala Phe Ser Thr Asp Asn Thr Glu Val Leu Ala Trp Ala Leu Glu  
 180 185 190  
 Asn Lys Gly Phe Glu Val Gly Ile Thr Ser Leu Gly Asp Pro Asp Thr  
 195 200 205  
 Ile Ala Ala Ala Val Gln Lys Gly Asn Gln Glu Leu Leu Asp Phe Ile  
 210 215 220  
 Asn Lys Asp Ile Glu Lys Leu Gly Lys Glu Asn Phe Phe His Lys Ala  
 225 230 235 240  
 Tyr Glu Lys Thr Leu His Pro Thr Tyr Gly Asp Ala Ala Lys Ala Asp  
 245 250 255  
 Asp Leu Val Val Glu Gly Gly Lys Val Asp  
 260 265

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCCAACATAT GGTAATCTG CGGATGGCAC AGTGACCATC GAGTATTTCA ACCAGAAAAA	60
AGAAATGACC AAAACCTTGG AAGAAATCAC TCGTGATTTT GAGAAGGAAA ACCCTAAGAT	120
CAAGGTCAAAA GTCGTCAATG TACCAAATGC TGGTGAAGTA TTGAAGACAC GCGTTCCTCGC	180
AGGAGATGTG CCTGATGTGG TCAATATTTA CCCACAGTCC ATCGAACTGC AAGAATGGGC	240
AAAAGCAGGT GTTTTTGAAG ATTTGAGCAA CAAAGACTAC CTGAAACGCG TGAAAAATGG	300

CTACGCTGAA AAATATGCTG TAAACGAAAA AGTTTACAAC GTTCCTTTTA CAGCTAATGC 360  
 TTATGGAATT TACTACAACA AAGATAAATT CGAAGAAGTG GGCTTGAAGG TTCCTGAAAC 420  
 CTGGGATGAA TTTGAACAGT TAGTCAAAGA TATCGTTGCT AAAGGACAAA CACCATTGTTG 480  
 AATTGCAGGT GCAGATGCTT GGACACTCAA TGGTTACAAT CAATTAGCCT TTGCGACAGC 540  
 AACAGGTGGA GGAAAAGAAG CAAATCAATA CCTTCGTTAT TCTCAACCAA ATGCCATTAA 600  
 ATTGTCGGAT CCGATTATGA AAGATGATAT CAAGGTCATG GACATCCTTC GCATCAATGG 660  
 ATCTAAGCAA AAGAACTGGG AAGGTGCTGG CTATACCGAT GTTATCGGAG CCTTCGCACG 720  
 TGGGGATGTC CTCATGACAC CAAATGGGTC TTGGGCGATC ACAGCGATTA ATGAACAAAA 780  
 ACCGAACTTT AAGATTGGGA CCTTCATGAT TCCAGGAAAA GAAAAAGGAC AAAGCTTAAC 840  
 CGTTGGTGCG GGAGACTTGG CATGGTCTAT CTCAGCCACC ACCAAACATC CAAAAGAAGC 900  
 CAATGCCCTTT GTGGAATATA TGACCCGTCC AGAAGTCATG CAAAAATACT ACGATGTGGA 960  
 CGGATCTCCA ACAGCGATCG AAGGGGTCAA ACAAGCAGGA GAAGATTCAC CGCTTGCTGG 1020  
 TATGACCGAA TATGCCTTTA CGGATCGTCA CTTGGTCTGG TTGCAACAAT ACTGGACCAG 1080  
 TGAAGCAGAC TTCCATACCT TGACCATGAA CTATGTCTTG ACCGGTGATA AACAAGGCAT 1140  
 GGTCAATGAT TTGAATGCCT TCTTTAACCC GATGAAAGCG GATGTGGAT 1189

(2) INFORMATION FOR SEQ ID NO:16:


(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Asn Tyr Gly Lys Ser Ala Asp Gly Thr Val Thr Ile Glu Tyr Phe  
 1 5 10 15  
 Asn Gln Lys Lys Glu Met Thr Lys Thr Leu Glu Glu Ile Thr Arg Asp  
 20 25 30  
 Phe Glu Lys Glu Asn Pro Lys Ile Lys Val Lys Val Val Asn Val Pro  
 35 40 45  
 Asn Ala Gly Glu Val Leu Lys Thr Arg Val Leu Ala Gly Asp Val Pro  
 50 55 60  
 Asp Val Val Asn Ile Tyr Pro Gln Ser Ile Glu Leu Gln Glu Trp Ala  
 65 70 75 80  
 Lys Ala Gly Val Phe Glu Asp Leu Ser Asn Lys Asp Tyr Leu Lys Arg  
 85 90 95  
 Val Lys Asn Gly Tyr Ala Glu Lys Tyr Ala Val Asn Glu Lys Val Tyr  
 100 105 110



Asn	Val	Pro	Phe	Thr	Ala	Asn	Ala	Tyr	Gly	Ile	Tyr	Tyr	Asn	Lys	Asp	115	120	125
Lys	Phe	Glu	Glu	Leu	Gly	Leu	Lys	Val	Pro	Glu	Thr	Trp	Asp	Glu	Phe	130	135	140
Glu	Gln	Leu	Val	Lys	Asp	Ile	Val	Ala	Lys	Gly	Gln	Thr	Pro	Phe	Gly	145	150	155
Ile	Ala	Gly	Ala	Asp	Ala	Trp	Thr	Leu	Asn	Gly	Tyr	Asn	Gln	Leu	Ala	165	170	175
Phe	Ala	Thr	Ala	Thr	Gly	Gly	Gly	Lys	Glu	Ala	Asn	Gln	Tyr	Leu	Arg	180	185	190
Tyr	Ser	Gln	Pro	Asn	Ala	Ile	Lys	Leu	Ser	Asp	Pro	Ile	Met	Lys	Asp	195	200	205
Asp	Ile	Lys	Val	Met	Asp	Ile	Leu	Arg	Ile	Asn	Gly	Ser	Lys	Gln	Lys	210	215	220
Asn	Trp	Glu	Gly	Ala	Gly	Tyr	Thr	Asp	Val	Ile	Gly	Ala	Phe	Ala	Arg	225	230	235
Gly	Asp	Val	Leu	Met	Thr	Pro	Asn	Gly	Ser	Trp	Ala	Ile	Thr	Ala	Ile	245	250	255
Asn	Glu	Gln	Lys	Pro	Asn	Phe	Lys	Ile	Gly	Thr	Phe	Met	Ile	Pro	Gly	260	265	270
Lys	Glu	Lys	Gly	Gln	Ser	Leu	Thr	Val	Gly	Ala	Gly	Asp	Leu	Ala	Trp	275	280	285
Ser	Ile	Ser	Ala	Thr	Thr	Lys	His	Pro	Lys	Glu	Ala	Asn	Ala	Phe	Val	290	295	300
Glu	Tyr	Met	Thr	Arg	Pro	Glu	Val	Met	Gln	Lys	Tyr	Tyr	Asp	Val	Asp	305	310	315
Gly	Ser	Pro	Thr	Ala	Ile	Glu	Gly	Val	Lys	Gln	Ala	Gly	Glu	Asp	Ser	325	330	335
Pro	Leu	Ala	Gly	Met	Thr	Glu	Tyr	Ala	Phe	Thr	Asp	Arg	His	Leu	Val	340	345	350
Trp	Leu	Gln	Gln	Tyr	Trp	Thr	Ser	Glu	Ala	Asp	Phe	His	Thr	Leu	Thr	355	360	365
Met	Asn	Tyr	Val	Leu	Thr	Gly	Asp	Lys	Gln	Gly	Met	Val	Asn	Asp	Leu	370	375	380
Asn	Ala	Phe	Phe	Asn	Pro	Met	Lys	Ala	Asp	Val	Asp					385	390	395

## (2) INFORMATION FOR SEQ ID NO: 17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:



TGGGAAAAAT TCTAGCGAAA CTAGTGGAGA TAATTGGTCA AAGTACCAGT CTAACAAGTC 60  
TATTACTATT GGATTTGATA GTACTTTTGT TCCAATGGGA TTTGCTCAGA AAGATGGTTC 120  
TTATGCAGGA TTTGATATTG ATTTAGCTAC AGCTGTTTTT GAAAAATACG GAATCACGGT 180  
AAATTGGCAA CCGATTGATT GGGATTTGAA AGAAGCTGAA TTGACAAAAG GAACGATTGA 240  
TCTGATTTGG AATGGCTATT CCGCTACAGA CGAACGCCGT GAAAAGGTGG CTTTCAGTAA 300  
CTCATATATG AAGAATGAGC AGGTATTGGT TACGAAGAAA TCATCTGGTA TCACGACTGC 360  
AAAGGATATG ACTGGAAAGA CATTAGGAGC TCAAGCTGGT TCATCTGGTT ATGCGGACTT 420  
TGAAGCAAAT CCAGAAATTT TGAAGAATAT TGTCGCTAAT AAGGAAGCGA ATCAATACCA 480  
AACCTTTAAT GAAGCCTTGA TTGATTTGAA AAACGATCGA ATTGATGGTC TATTGATTGA 540  
CCGTGTCCTAT GCAAACCTATT ATTTAGAAGC AGAAGGTGTT TTAAACGATT ATAATGTCTT 600  
TACAGTTGGA CTAGAAACAG AAGCTTTTGC GGTGGAGCC CGTAAGGAAG ATACAAACTT 660  
GGTTAAGAAG ATAAATGAAG CTTTTTCTAG TCTTTACAAG GACGGCAAGT TCCAAGAAAT 720  
CAGCCAAAAA TGGTTTGGAG AAGATGTAGC AACCAAAGAA GTAAAAGAAG GACAG 775

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Lys Asn Ser Ser Glu Thr Ser Gly Asp Asn Trp Ser Lys Tyr Gln  
1 5 10 15  
Ser Asn Lys Ser Ile Thr Ile Gly Phe Asp Ser Thr Phe Val Pro Met  
20 25 30  
Gly Phe Ala Gln Lys Asp Gly Ser Tyr Ala Gly Phe Asp Ile Asp Leu  
35 40 45  
Ala Thr Ala Val Phe Glu Lys Tyr Gly Ile Thr Val Asn Trp Gln Pro  
50 55 60  
Ile Asp Trp Asp Leu Lys Glu Ala Glu Leu Thr Lys Gly Thr Ile Asp  
65 70 75 80  
Leu Ile Trp Asn Gly Tyr Ser Ala Thr Asp Glu Arg Arg Glu Lys Val  
85 90 95  
Ala Phe Ser Asn Ser Tyr Met Lys Asn Glu Gln Val Leu Val Thr Lys  
100 105 110  
Lys Ser Ser Gly Ile Thr Thr Ala Lys Asp Met Thr Gly Lys Thr Leu  
115 120 125

Gly Ala Gln Ala Gly Ser Ser Gly Tyr Ala Asp Phe Glu Ala Asn Pro  
 130 135 140  
 Glu Ile Leu Lys Asn Ile Val Ala Asn Lys Glu Ala Asn Gln Tyr Gln  
 145 150 155 160  
 Thr Phe Asn Glu Ala Leu Ile Asp Leu Lys Asn Asp Arg Ile Asp Gly  
 165 170 175  
 Leu Leu Ile Asp Arg Val Tyr Ala Asn Tyr Tyr Leu Glu Ala Glu Gly  
 180 185 190  
 Val Leu Asn Asp Tyr Asn Val Phe Thr Val Gly Leu Glu Thr Glu Ala  
 195 200 205  
 Phe Ala Val Gly Ala Arg Lys Glu Asp Thr Asn Leu Val Lys Lys Ile  
 210 215 220  
 Asn Glu Ala Phe Ser Ser Leu Tyr Lys Asp Gly Lys Phe Gln Glu Ile  
 225 230 235 240  
 Ser Gln Lys Trp Phe Gly Glu Asp Val Ala Thr Lys Glu Val Lys Glu  
 245 250 255  
 Gly Gln

## (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGCTAGCGGA AAAAAAGATA CAACTTCTGG TCAAAAAC TA AAAGTTGTTG CTACAAACTC 60  
 AATCATCGCT GATATTACTA AAAATATTGC TGGTGACAAA ATTGACCTTC ATAGTATCGT 120  
 TCCGATTGGG CAAGACCCAC ACGAATACGA ACCACTTCCT GAAGACGTTA AGAAAACTTC 180  
 TGAGGCTAAT TTGATTTTCT ATAACGGTAT CAACCTTGAA ACAGGTGGCA ATGCTTGGTT 240  
 TACAAAATTG GTAGAAAATG CCAAGAAAAC TGAAAACAAA GACTACTTCG CAGTCAGCGA 300  
 CGGCGTTGAT GTTATCTACC TTGAAGGTCA AAATGAAAAA GGAAAAGAAG ACCCACACGC 360  
 TTGGCTTAAC CTTGAAAACG GTATTATTTT TGCTAAAAAT ATCGCCAAAC AATTGAGCGC 420  
 CAAAGACCCT AACAATAAAG AATTCTATGA AAAAAATCTC AAAGAATATA CTGATAAGTT 480  
 AGACAAACTT GATAAAGAAA GTAAGGATAA ATTTAATAAG ATCCCTGCTG AAAAGAACT 540  
 CATTGTAACC AGCGAAGGAG CATTCAAATA CTTCTCTAAA GCCTATGGTG TCCCAAGTGC 600  
 TTACATCTGG GAAATCAATA CTGAAGAAGA AGGAATCCT GAACAAATCA AGACCTTGGT 660  
 TGAAAAACTT CGCCAAACAA AAGTTCCATC ACTCTTTGTA GAATCAAGTG TGGATGACCG 720  
 TCCAATGAAA ACTGTTTCTC AAGACACAAA CATCCCAATC TACGCTCAAA TCTTTACTGA 780

CTCTATCGCA GAACAAGGTA AAGAAGGCGA CAGCTACTAC AGCATGATGA AATACAACCT

840

TGACAAGATT GCTGAAGGAT TGGCAAAA

868


(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:



Ala	Ser	Gly	Lys	Lys	Asp	Thr	Thr	Ser	Gly	Gln	Lys	Leu	Lys	Val	Val	1	5	10	15
Ala	Thr	Asn	Ser	Ile	Ile	Ala	Asp	Ile	Thr	Lys	Asn	Ile	Ala	Gly	Asp	20	25	30	
Lys	Ile	Asp	Leu	His	Ser	Ile	Val	Pro	Ile	Gly	Gln	Asp	Pro	His	Glu	35	40	45	
Tyr	Glu	Pro	Leu	Pro	Glu	Asp	Val	Lys	Lys	Thr	Ser	Glu	Ala	Asn	Leu	50	55	60	
Ile	Phe	Tyr	Asn	Gly	Ile	Asn	Leu	Glu	Thr	Gly	Gly	Asn	Ala	Trp	Phe	65	70	75	
Thr	Lys	Leu	Val	Glu	Asn	Ala	Lys	Lys	Thr	Glu	Asn	Lys	Asp	Tyr	Phe	85	90	95	
Ala	Val	Ser	Asp	Gly	Val	Asp	Val	Ile	Tyr	Leu	Glu	Gly	Gln	Asn	Glu	100	105	110	
Lys	Gly	Lys	Glu	Asp	Pro	His	Ala	Trp	Leu	Asn	Leu	Glu	Asn	Gly	Ile	115	120	125	
Ile	Phe	Ala	Lys	Asn	Ile	Ala	Lys	Gln	Leu	Ser	Ala	Lys	Asp	Pro	Asn	130	135	140	
Asn	Lys	Glu	Phe	Tyr	Glu	Lys	Asn	Leu	Lys	Glu	Tyr	Thr	Asp	Lys	Leu	145	150	155	
Asp	Lys	Leu	Asp	Lys	Glu	Ser	Lys	Asp	Lys	Phe	Asn	Lys	Ile	Pro	Ala	165	170	175	
Glu	Lys	Lys	Leu	Ile	Val	Thr	Ser	Glu	Gly	Ala	Phe	Lys	Tyr	Phe	Ser	180	185	190	
Lys	Ala	Tyr	Gly	Val	Pro	Ser	Ala	Tyr	Ile	Trp	Glu	Ile	Asn	Thr	Glu	195	200	205	
Glu	Glu	Gly	Thr	Pro	Glu	Gln	Ile	Lys	Thr	Leu	Val	Glu	Lys	Leu	Arg	210	215	220	
Gln	Thr	Lys	Val	Pro	Ser	Leu	Phe	Val	Glu	Ser	Ser	Val	Asp	Asp	Arg	225	230	235	
Pro	Met	Lys	Thr	Val	Ser	Gln	Asp	Thr	Asn	Ile	Pro	Ile	Tyr	Ala	Gln				

[illegible]

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1546 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TGGCTCAAAA	AATACAGCTT	CAAGTCCAGA	TTATAAGTTG	GAAGGTGTAA	CATTCCCGCT	60
TCAAGAAAAG	AAAACATTGA	AGTTTATGAC	AGCCAGTTCA	CCGTTATCTC	CTAAAGACCC	120
AAATGAAAAG	TTAATTTTGC	AACGTTTGGA	GAAGGAAACT	GGCGTTCATA	TTGACTGGAC	180
CAACTACCAA	TCCGACTTTG	CAGAAAAACG	TAACTTGGAT	ATTTCTAGTG	GTGATTTACC	240
AGATGCTATC	CACAACGACG	GAGCTTCAGA	TGTGGACTTG	ATGAAGTGGG	CTAAAAAAGG	300
TGTTATTATT	CCAGTTGAAG	ATTTGATTGA	TAAATACATG	CCAAATCTTA	AGAAAATTTT	360
GGATGAGAAA	CCAGAGTACA	AGGCCTTGAT	GACAGCACCT	GATGGGCACA	TTTACTCATT	420
TCCATGGATT	GAAGAGCTTG	GAGATGGTAA	AGAGTCTATT	CACAGTGTCA	ACGATATGGC	480
TTGGATTAAC	AAAGATTGGC	TTAAGAAACT	TGGTCTTGAA	ATGCCAAAAA	CTACTGATGA	540
TTTGATTAAA	GTCCTAGAAG	CTTTCAAAAA	CGGGGATCCA	AATGGAAATG	GAGAGGCTGA	600
TGAAATTCCA	TTTTCATTTA	TTAGTGGTAA	CGGAAACGAA	GATTTTAAAT	TCCTATTTGC	660
TGCATTTGGT	ATAGGGGATA	ACGATGATCA	TTTAGTAGTA	GGAAATGATG	GCAAAGTTGA	720
CTTCACAGCA	GATAACGATA	ACTATAAAGA	AGGTGTCAAA	TTTATCCGTC	AATTGCAAGA	780
AAAAGGCCTG	ATTGATAAAG	AAGCTTTTCGA	ACATGATTGG	AATAGTTACA	TTGCTAAAGG	840
TCATGATCAG	AAATTTGGTG	TTTACTTTAC	ATGGGATAAG	AATAATGTTA	CTGGAAGTAA	900
CGAAAGTTAT	GATGTTTTAC	CAGTACTTGC	TGGACCAAGT	GGTCAAAAAC	ACGTAGCTCG	960
TACAAACGGT	ATGGGATTTG	CACGTGACAA	GATGGTTATT	ACCAGTGTAA	ACAAAAACCT	1020
AGAATTGACA	GCTAAATGGA	TTGATGCACA	ATACGCTCCA	CTCCAATCTG	TGCAAAATAA	1080
CTGGGGAACT	TACGGAGATG	ACAAACAACA	AAACATCTTT	GAATTGGATC	AAGCGTCAAA	1140
TAGTCTAAAA	CACTTACCAC	TAAACGGAAC	TGCACCAGCA	GAACTTCGTC	AAAAGACTGA	1200
AGTAGGAGGA	CCACTAGCTA	TCCTAGATTC	ATACTATGGT	AAAGTAACAA	CCATGCCTGA	1260

TGATGCCAAA TGGCGTTTGG ATCTTATCAA AGAATATTAT GTTCCTTACA TGAGCAATGT 1320  
 CAATAACTAT CCAAGAGTCT TTATGACACA GGAAGATTG GACAAGATTG CCCATATCGA 1380  
 AGCAGATATG AATGACTATA TCTACCGTAA ACGTGCTGAA TGGATTGTAA ATGGCAATAT 1440  
 TGATACTGAG TGGGATGATT ACAAGAAAGA ACTTGAAAAA TACGGACTTT CTGATTACCT 1500  
 CGCTATTAAA CAAAAATACT ACGACCAATA CCAAGCAAAC AAAAAC 1546

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Ser Lys Asn Thr Ala Ser Ser Pro Asp Tyr Lys Leu Glu Gly Val  
 1 5 10 15  
 Thr Phe Pro Leu Gln Glu Lys Lys Thr Leu Lys Phe Met Thr Ala Ser  
 20 25 30  
 Ser Pro Leu Ser Pro Lys Asp Pro Asn Glu Lys Leu Ile Leu Gln Arg  
 35 40 45  
 Leu Glu Lys Glu Thr Gly Val His Ile Asp Trp Thr Asn Tyr Gln Ser  
 50 55 60  
 Asp Phe Ala Glu Lys Arg Asn Leu Asp Ile Ser Ser Gly Asp Leu Pro  
 65 70 75 80  
 Asp Ala Ile His Asn Asp Gly Ala Ser Asp Val Asp Leu Met Asn Trp  
 85 90 95  
 Ala Lys Lys Gly Val Ile Ile Pro Val Glu Asp Leu Ile Asp Lys Tyr  
 100 105 110  
 Met Pro Asn Leu Lys Lys Ile Leu Asp Glu Lys Pro Glu Tyr Lys Ala  
 115 120 125  
 Leu Met Thr Ala Pro Asp Gly His Ile Tyr Ser Phe Pro Trp Ile Glu  
 130 135 140  
 Glu Leu Gly Asp Gly Lys Glu Ser Ile His Ser Val Asn Asp Met Ala  
 145 150 155 160  
 Trp Ile Asn Lys Asp Trp Leu Lys Lys Leu Gly Leu Glu Met Pro Lys  
 165 170 175  
 Thr Thr Asp Asp Leu Ile Lys Val Leu Glu Ala Phe Lys Asn Gly Asp  
 180 185 190  
 Pro Asn Gly Asn Gly Glu Ala Asp Glu Ile Pro Phe Ser Phe Ile Ser  
 195 200 205  
 Gly Asn Gly Asn Glu Asp Phe Lys Phe Leu Phe Ala Ala Phe Gly Ile

210					215					220					
Gly 225	Asp	Asn	Asp	Asp	His 230	Leu	Val	Val	Gly	Asn 235	Asp	Gly	Lys	Val	Asp 240
Phe	Thr	Ala	Asp	Asn 245	Asp	Asn	Tyr	Lys	Glu 250	Gly	Val	Lys	Phe	Ile 255	Arg
Gln	Leu	Gln	Glu 260	Lys	Gly	Leu	Ile	Asp 265	Lys	Glu	Ala	Phe	Glu 270	His	Asp
Trp	Asn	Ser 275	Tyr	Ile	Ala	Lys	Gly 280	His	Asp	Gln	Lys	Phe 285	Gly	Val	Tyr
Phe 290	Thr	Trp	Asp	Lys	Asn	Asn 295	Val	Thr	Gly	Ser	Asn 300	Glu	Ser	Tyr	Asp
Val 305	Leu	Pro	Val	Leu	Ala 310	Gly	Pro	Ser	Gly	Gln 315	Lys	His	Val	Ala	Arg 320
Thr	Asn	Gly	Met	Gly 325	Phe	Ala	Arg	Asp	Lys 330	Met	Val	Ile	Thr	Ser 335	Val
Asn	Lys	Asn	Leu 340	Glu	Leu	Thr	Ala	Lys 345	Trp	Ile	Asp	Ala	Gln 350	Tyr	Ala
Pro	Leu	Gln 355	Ser	Val	Gln	Asn	Asn 360	Trp	Gly	Thr	Tyr	Gly 365	Asp	Asp	Lys
Gln 370	Gln	Asn	Ile	Phe	Glu	Leu 375	Asp	Gln	Ala	Ser	Asn 380	Ser	Leu	Lys	His
Leu 385	Pro	Leu	Asn	Gly	Thr 390	Ala	Pro	Ala	Glu	Leu 395	Arg	Gln	Lys	Thr	Glu 400
Val	Gly	Gly	Pro	Leu 405	Ala	Ile	Leu	Asp	Ser 410	Tyr	Tyr	Gly	Lys	Val 415	Thr
Thr	Met	Pro	Asp 420	Asp	Ala	Lys	Trp	Arg 425	Leu	Asp	Leu	Ile	Lys 430	Glu	Tyr
Tyr	Val	Pro 435	Tyr	Met	Ser	Asn	Val 440	Asn	Asn	Tyr	Pro	Arg 445	Val	Phe	Met
Thr	Gln 450	Glu	Asp	Leu	Asp	Lys 455	Ile	Ala	His	Ile	Glu 460	Ala	Asp	Met	Asn
Asp 465	Tyr	Ile	Tyr	Arg	Lys 470	Arg	Ala	Glu	Trp	Ile 475	Val	Asn	Gly	Asn	Ile 480
Asp	Thr	Glu	Trp	Asp 485	Asp	Tyr	Lys	Lys	Glu 490	Leu	Glu	Lys	Tyr	Gly 495	Leu
Ser	Asp	Tyr	Leu 500	Ala	Ile	Lys	Gln	Lys 505	Tyr	Tyr	Asp	Gln	Tyr 510	Gln	Ala
Asn	Lys	Asn 515													

## (2) INFORMATION FOR SEQ ID NO: 23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TAGTACAAAC TCAAGCACTA GTCAGACAGA GACCAGTAGC TCTGCTCCAA CAGAGGTAAC 60  
 CATTAAAAGT TCACTGGACG AGGTCAAAC TTTCAAAGTT CCTGAAAAGA TTGTGACCTT 120  
 TGACCTCGGC GCTGCGGATA CTATTCGCGC TTTAGGATTT GAAAAAATA TCGTCGGAAT 180  
 GCCTACAAAA ACTGTTCCGA CTTATCTAAA AGACCTAGTG GGAACGTGCA AAAATGTTGG 240  
 TTCTATGAAA GAACCTGATT TAGAAGCTAT CGCCGCCCTT GAGCCTGATT TGATTATCGC 300  
 TTCGCCACGT ACACAAAAAT TCGTAGACAA ATTCAAAGAA ATCGCCCCAA CCGTTCTCTT 360  
 CCAAGCAAGC AAGGACGACT ACTGGACTTC TACCAAGGCT AATATCGAAT CCTTAGCAAG 420  
 TGCCTTCGGC GAAACTGGTA CACAGAAAGC CAAGGAAGAA TTGACCAAGC TAGACAAGAG 480  
 CATCCAAGAA GTCGCTACTA AAAATGAAAG CTCTGACAAA AAAGCCCTTG CGATCCTCTT 540  
 TAATGAAGGA AAAATGGCAG CCTTTGGTGC CAAATCTCGT TTCTCTTTCT TGTACCAAAC 600  
 CTTGAAATTC AAACCAACTG ATACAAAATT TGAAGACTCA CGCCACGGAC AAGAAGTCAG 660  
 CTTTGAAAGT GTCAAAGAAA TCAACCCTGA CATCCTCTTT GTCATCAACC GTACCCCTTG 720  
 CATCGGTGGG GACAACTCTA GCAACGACGG TGTCTTAGAA AATGCCCTTA TCGCTGAAAC 780  
 ACCTGCTGCT AAAAATGGTA AGATTATCCA ACTAACACCA GACCTCTGGT ATCTAAGCGG 840  
 AGGCGGACTT GAATCAACAA AACTCATGAT TGAAGACATA CAAAAGCTT TGAAA 895


(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 298 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Thr Asn Ser Ser Thr Ser Gln Thr Glu Thr Ser Ser Ser Ala Pro  
 1 5 10 15  
 Thr Glu Val Thr Ile Lys Ser Ser Leu Asp Glu Val Lys Leu Ser Lys  
 20 25 30  
 Val Pro Glu Lys Ile Val Thr Phe Asp Leu Gly Ala Ala Asp Thr Ile  
 35 40 45  
 Arg Ala Leu Gly Phe Glu Lys Asn Ile Val Gly Met Pro Thr Lys Thr  
 50 55 60  
 Val Pro Thr Tyr Leu Lys Asp Leu Val Gly Thr Val Lys Asn Val Gly  
 65 70 75 80



Ser Met Lys Glu Pro Asp Leu Glu Ala Ile Ala Ala Leu Glu Pro Asp  
 85 90 95  
 Leu Ile Ile Ala Ser Pro Arg Thr Gln Lys Phe Val Asp Lys Phe Lys  
 100 105 110  
 Glu Ile Ala Pro Thr Val Leu Phe Gln Ala Ser Lys Asp Asp Tyr Trp  
 115 120 125  
 Thr Ser Thr Lys Ala Asn Ile Glu Ser Leu Ala Ser Ala Phe Gly Glu  
 130 135 140  
 Thr Gly Thr Gln Lys Ala Lys Glu Glu Leu Thr Lys Leu Asp Lys Ser  
 145 150 155 160  
 Ile Gln Glu Val Ala Thr Lys Asn Glu Ser Ser Asp Lys Lys Ala Leu  
 165 170 175  
 Ala Ile Leu Leu Asn Glu Gly Lys Met Ala Ala Phe Gly Ala Lys Ser  
 180 185 190  
 Arg Phe Ser Phe Leu Tyr Gln Thr Leu Lys Phe Lys Pro Thr Asp Thr  
 195 200 205  
 Lys Phe Glu Asp Ser Arg His Gly Gln Glu Val Ser Phe Glu Ser Val  
 210 215 220  
 Lys Glu Ile Asn Pro Asp Ile Leu Phe Val Ile Asn Arg Thr Leu Ala  
 225 230 235 240  
 Ile Gly Gly Asp Asn Ser Ser Asn Asp Gly Val Leu Glu Asn Ala Leu  
 245 250 255  
 Ile Ala Glu Thr Pro Ala Ala Lys Asn Gly Lys Ile Ile Gln Leu Thr  
 260 265 270  
 Pro Asp Leu Trp Tyr Leu Ser Gly Gly Gly Leu Glu Ser Thr Lys Leu  
 275 280 285  
 Met Ile Glu Asp Ile Gln Lys Ala Leu Lys  
 290 295

## (2) INFORMATION FOR SEQ ID NO: 25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TGGCAATTCT GGCGGAAGTA AAGATGCTGC CAAATCAGGT GGTGACGGTG CCAAAACAGA	60
AATCACTTGG TGGGCATTCC CAGTATTTAC CCAAGAAAAA ACTGGTGACG GTGTTGGAAC	120
TTATGAAAAA TCAATCATCG AAGCGTTTGA AAAAGCAAAC CCAGATATAA AAGTGAAATT	180
GGAAACCATC GACTTCAAGT CAGGTCCTGA AAAAATCACA ACAGCCATCG AAGCAGGAAC	240
AGCTCCAGAC GTACTCTTTG ATGCACCAGG ACGTATCATC CAATACGGTA AAAACGGTAA	300



ATTGGCTGAG TTGAATGACC TCTTCACAGA TGAATTTGTT AAAGATGTCA ACAATGAAAA 360  
CATCGTACAA GCAAGTAAAG CTGGAGACAA GGCTTATATG TATCCGATTA GTTCTGCCCC 420  
ATTCTACATG GCAATGAACA AGAAAATGTT AGAAGATGCT GGAGTAGCAA ACCTTGTAAG 480  
AGAAGGTTGG ACAACTGATG ATTTTGAAAA AGTATTGAAA GCACTTAAAG ACAAGGGTTA 540  
CACACCAGGT TCATTGTTCA GTTCTGGTCA AGGGGGAGAC CAAGGAACAC GTGCCTTTAT 600  
CTCTAACCTT TATAGCGGTT CTGTAACAGA TGAAAAAGTT AGCAAATATA CAACTGATGA 660  
TCCTAAATTC GTCAAAGGTC TTGAAAAAGC AACTAGCTGG ATTAAAGACA ATTTGATCAA 720  
TAATGGTTCA CAATTTGACG GTGGGGCAGA TATCCAAAAC TTTGCCAACG GTCAAACATC 780  
TTACACAATC CTTTGGGCAC CAGCTCAAAA TGGTATCCAA GCTAAACTTT TAGAAGCAAG 840  
TAAGGTAGAA GTGGTAGAAG TACCATTCCC ATCAGACGAA GGTAAGCCAG CTCTTGAGTA 900  
CCTTGTAAC GGGTTTGACG TATTCAACAA TAAAGACGAC AAGAAAGTCG CTGCATCTAA 960  
GAAATTCATC CAGTTTATCG CAGATGACAA GGAGTGGGGA CCTAAAGACG TAGTTCGTAC 1020  
AGGTGCTTTC CCAGTCCGTA CTTCAATTGG AAAACTTTAT GAAGACAAAC GCATGGAAAC 1080  
AATCAGCGGC TGGACTCAAT ACTACTCACC ATACTACAAC ACTATTGATG GATTTGCTGA 1140  
AATGAGAACA CTTTGGTTCC CAATGTTGCA ATCTGTATCA AATGGTGACG AAAAACCAGC 1200  
AGATGCTTTG AAAGCCTTCA CTGAAAAAGC GAACGAAACA ATCAAAAAAG CTATGAAACA 1260  
A 1261

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly Asn Ser Gly Gly Ser Lys Asp Ala Ala Lys Ser Gly Gly Asp Gly  
1 5 10 15  
Ala Lys Thr Glu Ile Thr Trp Trp Ala Phe Pro Val Phe Thr Gln Glu  
20 25 30  
Lys Thr Gly Asp Gly Val Gly Thr Tyr Glu Lys Ser Ile Ile Glu Ala  
35 40 45  
Phe Glu Lys Ala Asn Pro Asp Ile Lys Val Lys Leu Glu Thr Ile Asp  
50 55 60  
Phe Lys Ser Gly Pro Glu Lys Ile Thr Thr Ala Ile Glu Ala Gly Thr  
65 70 75 80  
Ala Pro Asp Val Leu Phe Asp Ala Pro Gly Arg Ile Ile Gln Tyr Gly

[illegible]

## (2) INFORMATION FOR SEQ ID NO: 27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TTCACAAGAA AAAACAAAAA ATGAAGATGG AGAAACTAAG ACAGAACAGA CAGCCAAAGC 60  
 TGATGGAACA GTCGGTAGTA AGTCTCAAGG AGCTGCCCAG AAGAAAGCAG AAGTGGTCAA 120  
 TAAAGGTGAT TACTACAGCA TTCAAGGGAA ATACGATGAA ATCATCGTAG CCAACAAACA 180  
 CTATCCATTG TCTAAAGACT ATAATCCAGG GGAAAATCCA ACAGCCAAGG CAGAGTTGGT 240  
 CAAACTCATC AAAGCGATGC AAGAGGCAGG TTTCCCTATT AGTGATCATT ACAGTGGTTT 300  
 TAGAAGTTAT GAAACTCAGA CCAAGCTCTA TCAAGATTAT GTCAACCAAG ATGGAAAGGC 360  
 AGCAGCTGAC CGTTACTCTG CCCGTCCTGG CTATAGCGAA CACCAGACAG GCTTGGCCTT 420  
 TGATGTGATT GGGACTGATG GTGATTTGGT GACAGAAGAA AAAGCAGCCC AATGGCTCTT 480  
 GGATCATGCA GCTGATTATG GCTTTGTTGT CCGTTATCTC AAAGGCAAGG AAAAGGAAAC 540  
 AGGCTATATG GCTGAAGAAT GGCACCTGCG TTATGTAGGA AAAGAAGCTA AAGAAATTGC 600  
 TGCAAGTGGT CTCAGTTTGG AAGAATACTA TGGCTTTGAA GGCGGAGACT ACGTCGAT 658

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Gln Glu Lys Thr Lys Asn Glu Asp Gly Glu Thr Lys Thr Glu Gln  
 1 5 10 15  
 Thr Ala Lys Ala Asp Gly Thr Val Gly Ser Lys Ser Gln Gly Ala Ala  
 20 25 30  
 Gln Lys Lys Ala Glu Val Val Asn Lys Gly Asp Tyr Tyr Ser Ile Gln  
 35 40 45  
 Gly Lys Tyr Asp Glu Ile Ile Val Ala Asn Lys His Tyr Pro Leu Ser  
 50 55 60  
 Lys Asp Tyr Asn Pro Gly Glu Asn Pro Thr Ala Lys Ala Glu Leu Val  
 65 70 75 80  
 Lys Leu Ile Lys Ala Met Gln Glu Ala Gly Phe Pro Ile Ser Asp His

				85						90						95			
Tyr	Ser	Gly	Phe	Arg	Ser	Tyr	Glu	Thr	Gln	Thr	Lys	Leu	Tyr	Gln	Asp				
			100					105					110						
Tyr	Val	Asn	Gln	Asp	Gly	Lys	Ala	Ala	Ala	Asp	Arg	Tyr	Ser	Ala	Arg				
		115					120					125							
Pro	Gly	Tyr	Ser	Glu	His	Gln	Thr	Gly	Leu	Ala	Phe	Asp	Val	Ile	Gly				
	130					135					140								
Thr	Asp	Gly	Asp	Leu	Val	Thr	Glu	Glu	Lys	Ala	Ala	Gln	Trp	Leu	Leu				
145					150					155					160				
Asp	His	Ala	Ala	Asp	Tyr	Gly	Phe	Val	Val	Arg	Tyr	Leu	Lys	Gly	Lys				
				165					170					175					
Glu	Lys	Glu	Thr	Gly	Tyr	Met	Ala	Glu	Glu	Trp	His	Leu	Arg	Tyr	Val				
			180					185					190						
Gly	Lys	Glu	Ala	Lys	Glu	Ile	Ala	Ala	Ser	Gly	Leu	Ser	Leu	Glu	Glu				
		195					200					205							
Tyr	Tyr	Gly	Phe	Glu	Gly	Gly	Asp	Tyr	Val	Asp									
	210					215													

## (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 790 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GAAAGGTCTG TGGTCAAATA ATCTTACCTG CGGTTATGAT GAAAAAATAA TCTTGGAAAA	60
TATAAATATA AAAATACCTG AAGAAAAAAT ATCAGTTATT ATTGGGTCAA ATGGTTGTGG	120
GAAATCAACA CTCATTAAAA CCTTGTCCTCG ACTTATAAAG CCATTAGAGG GAGAAGTATT	180
GCTTGATAAT AAATCAATTA ATTCTTATAA AGAAAAAGAT TTAGCAAAAC ACATAGCTAT	240
ATTACCTCAA TCTCCAATAA TCCCTGAATC AATAACAGTA GCTGATCTTG TAAGCCGTGG	300
TCGTTTCCCC TACAGAAAGC CTTTAAAGAG TCTTGGAAAA GATGACCTTG AAATAATAAA	360
CAGATCAATG GTTAAGGCCA ATGTTGAAGA TCTAGCAAAT AACCTAGTTG AAGAACTTTC	420
TGGGGGTCAA AGGCAAAGAG TATGGATAGC TCTAGCCCTA GCCCAAGATA CAAGTATCCT	480
ACTTTTAGAT GAGCCAACTA CTTACTTGGA TATCTCATAT CAAATAGAAC TATTAGACCT	540
CTTGACTGAT CTAAACCAAA AATATAAGAC AACCATTGTC ATGATTTTGC ACGATATAAA	600
TCTAACAGCA AGATACGCTG ATTACCTATT TGCAATTAAA GAAGGTAAAC TTGTTGCAGA	660
GGGAAAGCCT GAAGATATAC TAAATGATAA ACTAGTTAAA GATATCTTTA ATCTTGAAGC	720
AAAAATTATA CGTGACCCTA TTTCCAATTC GCCTCTAATG ATTCCTATTG GCAAGCACCA	780

TGTTAACTCT


790

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 262 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:



Lys Gly Leu Trp Ser Asn Asn Leu Thr Cys Gly Tyr Asp Glu Lys Ile  
 1 5 10 15  
 Ile Leu Glu Asn Ile Asn Ile Lys Ile Pro Glu Glu Lys Ile Ser Val  
 20 25 30  
 Ile Ile Gly Ser Asn Gly Cys Gly Lys Ser Thr Leu Ile Lys Thr Leu  
 35 40 45  
 Ser Arg Leu Ile Lys Pro Leu Glu Gly Glu Val Leu Leu Asp Asn Lys  
 50 55 60  
 Ser Ile Asn Ser Tyr Lys Glu Lys Asp Leu Ala Lys His Ile Ala Ile  
 65 70 75 80  
 Leu Pro Gln Ser Pro Ile Ile Pro Glu Ser Ile Thr Val Ala Asp Leu  
 85 90 95  
 Val Ser Arg Gly Arg Phe Pro Tyr Arg Lys Pro Phe Lys Ser Leu Gly  
 100 105 110  
 Lys Asp Asp Leu Glu Ile Ile Asn Arg Ser Met Val Lys Ala Asn Val  
 115 120 125  
 Glu Asp Leu Ala Asn Asn Leu Val Glu Glu Leu Ser Gly Gly Gln Arg  
 130 135 140  
 Gln Arg Val Trp Ile Ala Leu Ala Leu Ala Gln Asp Thr Ser Ile Leu  
 145 150 155 160  
 Leu Leu Asp Glu Pro Thr Thr Tyr Leu Asp Ile Ser Tyr Gln Ile Glu  
 165 170 175  
 Leu Leu Asp Leu Leu Thr Asp Leu Asn Gln Lys Tyr Lys Thr Thr Ile  
 180 185 190  
 Cys Met Ile Leu His Asp Ile Asn Leu Thr Ala Arg Tyr Ala Asp Tyr  
 195 200 205  
 Leu Phe Ala Ile Lys Glu Gly Lys Leu Val Ala Glu Gly Lys Pro Glu  
 210 215 220  
 Asp Ile Leu Asn Asp Lys Leu Val Lys Asp Ile Phe Asn Leu Glu Ala  
 225 230 235 240  
 Lys Ile Ile Arg Asp Pro Ile Ser Asn Ser Pro Leu Met Ile Pro Ile  
 245 250 255  
 Gly Lys His His Val Ser

260

## (2) INFORMATION FOR SEQ ID NO: 31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AAACTCAGAA AAGAAAGCAG ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG 60  
 CGGTTCTGAA GAAAAACGTT GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATTAC 120  
 CTTGGAATTT ACAGAGTTCA CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA 180  
 AGTAGATTTG AACGCTTTCC AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG 240  
 AAAAGACCTT GTAGCGATTG CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT 300  
 GAATGGAAGT GCCAACAAGT AACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC 360  
 TGTACCGAAT GACGCTACAA ACGAAAGCCG TGCGCTTTAT TTGCTTCAAT CAGCTGGCTT 420  
 GATTAAATTG GATGTTTCTG GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC 480  
 AAAGAACTTG AAAATCACTG AATTGGACGC TAGCCAAACA GTCGTTTCAT TGTCATCAGT 540  
 TGACGCTGCC GTTGTAACA ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC 600  
 ACTTTTCAAA GAACAAGCTG ATGAAAATC AAAACAATGG TACAACATCA TTGTTGCAAA 660  
 AAAAGATTGG GAAACATCAC CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA 720  
 CACAGATGAC GTGAAAAAAG TTATCGAAGA ATCATCAGAT GGTTTGGATC AACCAGTTTG 780  
 G 781

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn Ser Glu Lys Lys Ala Asp Asn Ala Thr Thr Ile Lys Ile Ala Thr  
 1 5 10 15  
 Val Asn Arg Ser Gly Ser Glu Glu Lys Arg Trp Asp Lys Ile Gln Glu  
 20 25 30  
 Leu Val Lys Lys Asp Gly Ile Thr Leu Glu Phe Thr Glu Phe Thr Asp  
 35 40 45

Tyr Ser Gln Pro Asn Lys Ala Thr Ala Asp Gly Glu Val Asp Leu Asn  
 50 55 60  
 Ala Phe Gln His Tyr Asn Phe Leu Asn Asn Trp Asn Lys Glu Asn Gly  
 65 70 75 80  
 Lys Asp Leu Val Ala Ile Ala Asp Thr Tyr Ile Ser Pro Ile Arg Leu  
 85 90 95  
 Tyr Ser Gly Leu Asn Gly Ser Ala Asn Lys Tyr Thr Lys Val Glu Asp  
 100 105 110  
 Ile Pro Ala Asn Gly Glu Ile Ala Val Pro Asn Asp Ala Thr Asn Glu  
 115 120 125  
 Ser Arg Ala Leu Tyr Leu Leu Gln Ser Ala Gly Leu Ile Lys Leu Asp  
 130 135 140  
 Val Ser Gly Thr Ala Leu Ala Thr Val Ala Asn Ile Lys Glu Asn Pro  
 145 150 155 160  
 Lys Asn Leu Lys Ile Thr Glu Leu Asp Ala Ser Gln Thr Ala Arg Ser  
 165 170 175  
 Leu Ser Ser Val Asp Ala Ala Val Val Asn Asn Thr Phe Val Thr Glu  
 180 185 190  
 Ala Lys Leu Asp Tyr Lys Lys Ser Leu Phe Lys Glu Gln Ala Asp Glu  
 195 200 205  
 Asn Ser Lys Gln Trp Tyr Asn Ile Ile Val Ala Lys Lys Asp Trp Glu  
 210 215 220  
 Thr Ser Pro Lys Ala Asp Ala Ile Lys Lys Val Ile Ala Ala Tyr His  
 225 230 235 240  
 Thr Asp Asp Val Lys Lys Val Ile Glu Glu Ser Ser Asp Gly Leu Asp  
 245 250 255  
 Gln Pro Val Trp  
 260

## (2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 640 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TTCGAAAGGG TCAGAAGGTG CAGACCTTAT CAGCATGAAA GGGGATGTCA TTACAGAACA	60
TCAATTTTAT GAGCAAGTGA AAAGCAACCC TTCAGCCCAA CAAGTCTTGT TAAATATGAC	120
CATCCAAAAA GTTTTTGAAA AACAAATATGG CTCAGAGCTT GATGATAAAG AGGTTGATGA	180
TACTATTGCC GAAGAAAAAA AACAAATATGG CGAAACTAC CAACGTGTCT TGTACAAGC	240
AGGTATGACT CTTGAAACAC GTAAAGCTCA AATTCGTACA AGTAAATTAG TTGAGTTGGC	300

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AGTTAAGAAG GTAGCAGAAG CTGAATTGAC AGATGAAGCC TATAAGAAAG CCTTTGATGA      360
GTACACTCCA GATGTAACGG CTCAAATCAT CCGTCTTAAT AATGAAGATA AGGCCAAAGA      420
AGTTCTCGAA AAAGCCAAGG CAGAAGGTGC TGATTTTGCT CAATTAGCCA AAGATAATTC      480
AACTGATGAA AAAACAAAAG AAAATGGTGG AGAAATTACC TTTGATTCTG CTTCACAGA      540
AGTACCTGGA GCAAGTCCAA AAAAGCCGCT TTTCGCTTTT AGATGTGGGA TGGTGTCTTCT      600
GGATGTGGAT TACAGCAACT GGGGCACACC AAGCCTACAG      640

```


## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:



```

Ser Lys Gly Ser Glu Gly Ala Asp Leu Ile Ser Met Lys Gly Asp Val
1           5           10           15
Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys Ser Asn Pro Ser Ala
          20           25           30
Gln Gln Val Leu Leu Asn Met Thr Ile Gln Lys Val Phe Glu Lys Gln
          35           40           45
Tyr Gly Ser Glu Leu Asp Asp Lys Glu Val Asp Asp Thr Ile Ala Glu
          50           55           60
Glu Lys Lys Gln Tyr Gly Glu Asn Tyr Gln Arg Val Leu Ser Gln Ala
          65           70           75           80
Gly Met Thr Leu Glu Thr Arg Lys Ala Gln Ile Arg Thr Ser Lys Leu
          85           90           95
Val Glu Leu Ala Val Lys Lys Val Ala Glu Ala Glu Leu Thr Asp Glu
          100          105          110
Ala Tyr Lys Lys Ala Phe Asp Glu Tyr Thr Pro Asp Val Thr Ala Gln
          115          120          125
Ile Ile Arg Leu Asn Asn Glu Asp Lys Ala Lys Glu Val Leu Glu Lys
          130          135          140
Ala Lys Ala Glu Gly Ala Asp Phe Ala Gln Leu Ala Lys Asp Asn Ser
          145          150          155          160
Thr Asp Glu Lys Thr Lys Glu Asn Gly Gly Glu Ile Thr Phe Asp Ser
          165          170          175
Ala Ser Thr Glu Val Pro Gly Ala Ser Pro Lys Lys Pro Leu Phe Ala
          180          185          190
Phe Arg Cys Gly Met Val Phe Leu Asp Val Asp Tyr Ser Asn Trp Gly
          195          200          205

```



Thr Pro Ser Leu Gln  
210

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 631 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GGGGATGGCA GCTTTTAAAA ATCCTAACAA TCAATACAAA GCTATTACAA TTGCTCAAAC	60
TCTAGGTGAT GATGCTTCTT CAGAGGAATT GGCTGGTAGA TATGGTTCTG CTGTTTCAGTG	120
TACAGAAAGTG ACTGCCTCAA ACCTTTCAAC AGTTAAACT AAAGCTACGG TTGTAGAAAA	180
ACCACTGAAA GATTTTAGAG CGTCTACGTC TGATCAGTCT GGTGGGTGG AATCTAATGG	240
TAAATGGTAT TTCTATGAGT CTGGTGATGT GAAGACAGGT TGGGTGAAAA CAGATGGTAA	300
ATGGTACTAT TTGAATGACT TAGGTGTCAT GCAGACTGGA TTTGTAAAAT TTTCTGGTAG	360
CTGGTATTAC TTGAGCAATT CAGGTGCTAT GTTTACAGGC TGGGGAACAG ATGGTAGCAG	420
ATGGTTCTAC TTTGACGGCT CAGGAGCTAT GAAGACAGGC TGGTACAAGG AAAATGGCAC	480
TTGGTATTAC CTTGACGAAG CAGGTATCAT GAAGACAGGT TGGTTTAAAG TCGGACCACA	540
CTGGTACTAT GCCTACGGTT CAGGAGCTTT GGCTGTGAGC ACAACAACAC CAGATGGTTA	600
CCGTGTAAAT GGTAATGGTG AATGGGTAAA C	631

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 210 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Met Ala Ala Phe Lys Asn Pro Asn Asn Gln Tyr Lys Ala Ile Thr	
1 5 10 15	
Ile Ala Gln Thr Leu Gly Asp Asp Ala Ser Ser Glu Glu Leu Ala Gly	
20 25 30	
Arg Tyr Gly Ser Ala Val Gln Cys Thr Glu Val Thr Ala Ser Asn Leu	
35 40 45	
Ser Thr Val Lys Thr Lys Ala Thr Val Val Glu Lys Pro Leu Lys Asp	
50 55 60	
Phe Arg Ala Ser Thr Ser Asp Gln Ser Gly Trp Val Glu Ser Asn Gly	
65 70 75 80	

Lys Trp Tyr Phe Tyr Glu Ser Gly Asp Val Lys Thr Gly Trp Val Lys  
 85 90 95  
 Thr Asp Gly Lys Trp Tyr Tyr Leu Asn Asp Leu Gly Val Met Gln Thr  
 100 105 110  
 Gly Phe Val Lys Phe Ser Gly Ser Trp Tyr Tyr Leu Ser Asn Ser Gly  
 115 120 125  
 Ala Met Phe Thr Gly Trp Gly Thr Asp Gly Ser Arg Trp Phe Tyr Phe  
 130 135 140  
 Asp Gly Ser Gly Ala Met Lys Thr Gly Trp Tyr Lys Glu Asn Gly Thr  
 145 150 155 160  
 Trp Tyr Tyr Leu Asp Glu Ala Gly Ile Met Lys Thr Gly Trp Phe Lys  
 165 170 175  
 Val Gly Pro His Trp Tyr Tyr Ala Tyr Gly Ser Gly Ala Leu Ala Val  
 180 185 190  
 Ser Thr Thr Thr Pro Asp Gly Tyr Arg Val Asn Gly Asn Gly Glu Trp  
 195 200 205  
 Val Asn  
 210

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1360 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AGACGAGCAA AAAATTAAGC AAGCAGAAGC GGAAGTTGAG AGTAAACAAG CTGAGGCTAC	60
AAGGTTAAAA AAAATCAAGA CAGATCGTGA AGAAGCAGAA GAAGAAGCTA AACGAAGAGC	120
AGATGCTAAA GAGCAAGGTA AACCAAAGGG GCGGGCAAAA CGAGGAGTTC CTGGAGAGCT	180
AGCAACACCT GATAAAAAAG AAAATGATGC GAAGTCTTCA GATTCTAGCG TAGGTGAAGA	240
AACTCTTCCA AGCCCATCCC TGAAACCAGA AAAAAAGGTA GCAGAAGCTG AGAAGAAGGT	300
TGAAGAAGCT AAGAAAAAG CCGAGGATCA AAAAGAAGAA GATCGCCGTA ACTACCCAAC	360
CAATACTTAC AAAACGCTTG AACTTGAAAT TGCTGAGTCC GATGTGGAAG TTAAAAAAGC	420
GGAGCTTGAA CTAGTAAAAG AGGAAGCTAA GGAACCTCGA AACGAGGAAA AAGTTAAGCA	480
AGCAAAAGCG GAAGTTGAGA GTAAAAAAGC TGAGGCTACA AGGTTAGAAA AAATCAAGAC	540
AGATCGTAAA AAAGCAGAAG AAGAAGCTAA ACGAAAAGCA GCAGAAGAAG ATAAAGTTAA	600
AGAAAAACCA GCTGAACAAC CACAACCAGC GCCGGCTCCA AAAGCAGAAA AACCAGCTCC	660
AGCTCCAAAA CCAGAGAATC CAGCTGAACA ACCAAAAGCA GAAAAACCAG CTGATCAACA	720

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AGCTGAAGAA GACTATGCTC GTAGATCAGA AGAAGAATAT AATCGCTTGA CTCAACAGCA      780
ACCGCCAAAA ACTGAAAAAC CAGCACAACC ATCTACTCCA AAAACAGGCT GGAAACAAGA      840
AAACGGTATG TGGTACTTCT ACAATACTGA TGGTTCAATG GCGACAGGAT GGCTCCAAAA      900
CAATGGCTCA TGGTACTACC TCAACAGCAA TGGCGCTATG GCGACAGGAT GGCTCCAAAA      960
CAATGGTTCA TGGTACTATC TAAACGCTAA TGGTTCAATG GCAACAGGAT GGCTCCAAAA     1020
CAATGGTTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA     1080
CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA     1140
CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTGATATG GCGACAGGTT GGGTGAAAGA     1200
TGGAGATACC TGGTACTATC TTGAAGCATC AGGTGCTATG AAAGCAAGCC AATGGTTCAA     1260
AGTATCAGAT AAATGGTACT ATGTCAATGG CTCAGGTGCC CTTGCAGTCA ACACAACTGT     1320
AGATGGCTAT GGAGTCAATG CCAATGGTGA ATGGGTAAAC                             1360

```

## (2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 453 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:



```

Asp Glu Gln Lys Ile Lys Gln Ala Glu Ala Glu Val Glu Ser Lys Gln
1           5           10
Ala Glu Ala Thr Arg Leu Lys Lys Ile Lys Thr Asp Arg Glu Glu Ala
20          25          30
Glu Glu Glu Ala Lys Arg Arg Ala Asp Ala Lys Glu Gln Gly Lys Pro
35          40          45
Lys Gly Arg Ala Lys Arg Gly Val Pro Gly Glu Leu Ala Thr Pro Asp
50          55          60
Lys Lys Glu Asn Asp Ala Lys Ser Ser Asp Ser Ser Val Gly Glu Glu
65          70          75          80
Thr Leu Pro Ser Pro Ser Leu Lys Pro Glu Lys Lys Val Ala Glu Ala
85          90          95
Glu Lys Lys Val Glu Glu Ala Lys Lys Lys Ala Glu Asp Gln Lys Glu
100         105         110
Glu Asp Arg Arg Asn Tyr Pro Thr Asn Thr Tyr Lys Thr Leu Glu Leu
115         120         125
Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu Glu Leu
130         135         140
Val Lys Glu Glu Ala Lys Glu Pro Arg Asn Glu Glu Lys Val Lys Gln
145         150         155         160

```

Ala Lys Ala Glu Val Glu Ser Lys Lys Ala Glu Ala Thr Arg Leu Glu  
 165 170 175  
 Lys Ile Lys Thr Asp Arg Lys Lys Ala Glu Glu Glu Ala Lys Arg Lys  
 180 185 190  
 Ala Ala Glu Glu Asp Lys Val Lys Glu Lys Pro Ala Glu Gln Pro Gln  
 195 200 205  
 Pro Ala Pro Ala Pro Lys Ala Glu Lys Pro Ala Pro Ala Pro Lys Pro  
 210 215 220  
 Glu Asn Pro Ala Glu Gln Pro Lys Ala Glu Lys Pro Ala Asp Gln Gln  
 225 230 235 240  
 Ala Glu Glu Asp Tyr Ala Arg Arg Ser Glu Glu Glu Tyr Asn Arg Leu  
 245 250 255  
 Thr Gln Gln Gln Pro Pro Lys Thr Glu Lys Pro Ala Gln Pro Ser Thr  
 260 265 270  
 Pro Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn  
 275 280 285  
 Thr Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp  
 290 295 300  
 Tyr Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Asn  
 305 310 315 320  
 Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser Met Ala Thr Gly  
 325 330 335  
 Trp Leu Gln Asn Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser  
 340 345 350  
 Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn  
 355 360 365  
 Ala Asn Gly Ser Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp  
 370 375 380  
 Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Val Lys Asp  
 385 390 395 400  
 Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser  
 405 410 415  
 Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Ser Gly  
 420 425 430  
 Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Gly Val Asn Ala Asn  
 435 440 445  
 Gly Glu Trp Val Asn  
 450

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGTGGTGAG GAAGAACTA AAAAGACTCA AGCAGCACAA CAGCCAAAAC AACAAACGAC	60
TGTACAACAA ATTGCTGTTG GAAAAGATGC TCCAGACTTC ACATTGCAAT CCATGGATGG	120
CAAAGAAGTT AAGTTATCTG ATTTTAAGGG TAAAAAGGTT TACTTGAAGT TTTGGGCTTC	180
ATGGTGTGGT CCATGCAAGA AAAGTATGCC AGAGTTGATG GAACTAGCGG CGAAACCAGA	240
TCGTGATTTT GAAATTCTTA CTGTCATTGC ACCAGGAATT CAAGGTGAAA AAAGTGTGTA	300
GCAATTCCCA CAATGGTTCC AGGAACAAGG ATATAAGGAT ATCCAGTTC TTTATGATAC	360
CAAAGCAACC ACTTCCAAGC TTATCAAATT CGAAGCATTC CTACAGAATA TT	412


(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:



Cys Gly Glu Glu Glu Thr Lys Lys Thr Gln Ala Ala Gln Gln Pro Lys	1 5 10 15
Gln Gln Thr Thr Val Gln Gln Ile Ala Val Gly Lys Asp Ala Pro Asp	20 25 30
Phe Thr Leu Gln Ser Met Asp Gly Lys Glu Val Lys Leu Ser Asp Phe	35 40 45
Lys Gly Lys Lys Val Tyr Leu Lys Phe Trp Ala Ser Trp Cys Gly Pro	50 55 60
Cys Lys Lys Ser Met Pro Glu Leu Met Glu Leu Ala Ala Lys Pro Asp	65 70 75 80
Arg Asp Phe Glu Ile Leu Thr Val Ile Ala Pro Gly Ile Gln Gly Glu	85 90 95
Lys Thr Val Glu Gln Phe Pro Gln Trp Phe Gln Glu Gln Gly Tyr Lys	100 105 110
Asp Ile Pro Val Leu Tyr Asp Thr Lys Ala Thr Thr Ser Lys Leu Ile	115 120 125
Lys Phe Glu Ala Phe Leu Gln Asn Ile	130 135

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1462 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GACTTTTAAAC AATAAACTA TTGAAGAGTT GCACAATCTC CTTGTCTCTA AGGAAATTTT	60
TGCAACAGAA TTGACCCAAG CAACACTTGA AAATATCAAG TCTCGTGAGG AAGCCCTCAA	120
TTCATTTGTC ACCATCGCTG AGGAGCAAGC TC'TTGTTCAA GCTAAAGCCA TTGATGAAGC	180
tGGAATTGAT GCTGACAATG TCCTTTTCAGG AATTCCACTT GCTGTTAAGG ATAACATCTC	240
TACAGACGGT ATTCTCACAA CTGCTGCCTC AAAAATGCTC TACAACTATG AGCCAATCTT	300
TGATGCGACa gCTgTTGCCA ATGCAAAAAC CAAGGGCATG ATTGTCGTTG GAAAGACCAA	360
CATGGACGAA TTTGCTATGG GTGGTTCAGG tGAAACTTCA CACTACGGAG CAACTAAAAA	420
CGCTTGGAAC CACAGCAAGG TTCCTGGTGG GTCATCAAGT GGTTCCTGCCG CAGCTGTAGC	480
CTCAGGACAA GTTCGCTTGT CACTTGGTTC TGATACTGGT GGTTCATCC GCCAACCTGC	540
TGCCTTCAAC GGAATCGTTG GTCTCAAACC AACCTACGGA ACAGTTTCAC GTTTCGGTCT	600
CATTGCCTTT GGTAGCTCAT TAGACCAGAT TGGACCTTTT GCTCCTACTG TTAAGGAAAA	660
TGCCCTCTTG CTCAACGCTA TTGCCAGCGA AGATGCTAAA GACTCTACTT CTGCTCCTGT	720
CCGCATCGCC GACTTTACTT CAAAAATCGG CCAAGACATC AAGGGTATGA AAATCGCTTT	780
GCCTAAGGAA TACCTAGGCG AAGGAATTGA TCCAGAGGTT AAGGAAACAA TCTTAAACGC	840
GGCCAAACAC TTTGAAAAAT TGGGTGCTAT CGTCGAAGAA GTCAGCCTTC CTCACTCTAA	900
ATACGGTGTT GCCGTTTATT ACATCATCGC TTCATCAGAA GCTTCATCAA ACTTGCAACG	960
CTTCGACGGT ATCCGTTACG GCTATCGCGC AGAAGATGCA ACCAACCTTG ATGAAATCTA	1020
TGTAAACAGC CGAAGCCAAG GTTTTGGTGA AGAGGTAAAA CGTCGTATCA TGCTGGGTAC	1080
TTTCAGTCTT TCATCAGGTT ACTATGATGC CTACTACAAA AAGGCTGGTC AAGTCCGTAC	1140
CCTCATCATT CAAGATTTTCG AAAAAGTCTT CGCGGATTAC GATTTGATTT TGGGTCCAAC	1200
TGCTCCAAGT GTTGCCATAG ACTTGGATTC TCTCAACCAT GACCCAGTTG CCATGTACTT	1260
AGCCGACCTA TTGACCATAC CTGTAAACTT GGCAGGACTG CCTGGAATTT CGATTCCCTGC	1320
TGGATTCTCT CAAGGTCTAC CTGTCGGACT CCAATTGATT GGTCCCAAGT ACTCTGAGGA	1380
AACCATTTAC CAAGCTGCTG CTGCTTTTGA AGCAACAACA GACTACCACA AACAACAACC	1440
CGTGATTTTT GGAGGTGACA AC	1462

(2) INFORMATION FOR SEQ ID NO:42:


(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:



Thr	Phe	Asn	Asn	Lys	Thr	Ile	Glu	Glu	Leu	His	Asn	Leu	Leu	Val	Ser	1	5	10	15
Lys	Glu	Ile	Ser	Ala	Thr	Glu	Leu	Thr	Gln	Ala	Thr	Leu	Glu	Asn	Ile	20	25	30	
Lys	Ser	Arg	Glu	Glu	Ala	Leu	Asn	Ser	Phe	Val	Thr	Ile	Ala	Glu	Glu	35	40	45	
Gln	Ala	Leu	Val	Gln	Ala	Lys	Ala	Ile	Asp	Glu	Ala	Gly	Ile	Asp	Ala	50	55	60	
Asp	Asn	Val	Leu	Ser	Gly	Ile	Pro	Leu	Ala	Val	Lys	Asp	Asn	Ile	Ser	65	70	75	80
Thr	Asp	Gly	Ile	Leu	Thr	Thr	Ala	Ala	Ser	Lys	Met	Leu	Tyr	Asn	Tyr	85	90	95	
Glu	Pro	Ile	Phe	Asp	Ala	Thr	Ala	Val	Ala	Asn	Ala	Lys	Thr	Lys	Gly	100	105	110	
Met	Ile	Val	Val	Gly	Lys	Thr	Asn	Met	Asp	Glu	Phe	Ala	Met	Gly	Gly	115	120	125	
Ser	Gly	Glu	Thr	Ser	His	Tyr	Gly	Ala	Thr	Lys	Asn	Ala	Trp	Asn	His	130	135	140	
Ser	Lys	Val	Pro	Gly	Gly	Ser	Ser	Ser	Gly	Ser	Ala	Ala	Ala	Val	Ala	145	150	155	160
Ser	Gly	Gln	Val	Arg	Leu	Ser	Leu	Gly	Ser	Asp	Thr	Gly	Gly	Ser	Ile	165	170	175	
Arg	Gln	Pro	Ala	Ala	Phe	Asn	Gly	Ile	Val	Gly	Leu	Lys	Pro	Thr	Tyr	180	185	190	
Gly	Thr	Val	Ser	Arg	Phe	Gly	Leu	Ile	Ala	Phe	Gly	Ser	Ser	Leu	Asp	195	200	205	
Gln	Ile	Gly	Pro	Phe	Ala	Pro	Thr	Val	Lys	Glu	Asn	Ala	Leu	Leu	Leu	210	215	220	
Asn	Ala	Ile	Ala	Ser	Glu	Asp	Ala	Lys	Asp	Ser	Thr	Ser	Ala	Pro	Val	225	230	235	240
Arg	Ile	Ala	Asp	Phe	Thr	Ser	Lys	Ile	Gly	Gln	Asp	Ile	Lys	Gly	Met	245	250	255	
Lys	Ile	Ala	Leu	Pro	Lys	Glu	Tyr	Leu	Gly	Glu	Gly	Ile	Asp	Pro	Glu	260	265	270	
Val	Lys	Glu	Thr	Ile	Leu	Asn	Ala	Ala	Lys	His	Phe	Glu	Lys	Leu	Gly	275	280	285	
Ala	Ile	Val	Glu	Glu	Val	Ser	Leu	Pro	His	Ser	Lys	Tyr	Gly	Val	Ala	290	295	300	

Val Tyr Tyr Ile Ile Ala Ser Ser Glu Ala Ser Ser Asn Leu Gln Arg  
305 310 315 320

Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Ala Glu Asp Ala Thr Asn Leu  
325 330 335

Asp Glu Ile Tyr Val Asn Ser Arg Ser Gln Gly Phe Gly Glu Glu Val  
340 345 350

Lys Arg Arg Ile Met Leu Gly Thr Phe Ser Leu Ser Ser Gly Tyr Tyr  
355 360 365

Asp Ala Tyr Tyr Lys Lys Ala Gly Gln Val Arg Thr Leu Ile Ile Gln  
370 375 380

Asp Phe Glu Lys Val Phe Ala Asp Tyr Asp Leu Ile Leu Gly Pro Thr  
385 390 395 400

Ala Pro Ser Val Ala Tyr Asp Leu Asp Ser Leu Asn His Asp Pro Val  
405 410 415

Ala Met Tyr Leu Ala Asp Leu Leu Thr Ile Pro Val Asn Leu Ala Gly  
420 425 430

Leu Pro Gly Ile Ser Ile Pro Ala Gly Phe Ser Gln Gly Leu Pro Val  
435 440 445

Gly Leu Gln Leu Ile Gly Pro Lys Tyr Ser Glu Glu Thr Ile Tyr Gln  
450 455 460

Ala Ala Ala Ala Phe Glu Ala Thr Thr Asp Tyr His Lys Gln Gln Pro  
465 470 475 480

Val Ile Phe Gly Gly Asp Asn  
485

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 433 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTTTACAGGT AAACAAC TAC AAGTCGGCGA CAAGGCGCTT GATTTTTCTC TTACTACAAC	60
AGATCTTTCT AAAAAATCTC TGGCTGATTT TGATGGCAAG AAAAAAGTCT TGAGTGTCGT	120
TCCTTCTATC GATACAGGCA TCTGCTCAAC TCAAACACGT CGTTTTAATG AAGAATTGGC	180
TGGACTGGAC AACACGGTCG TATTGACTGT TTCAATGGAC CTACCTTTTG CTCAAAAACG	240
TTGGTGCGGT GCTGAAGGCC TTGACAATGC CATTATGCTT TCAGACTACT TTGACCATTC	300
TTTCGGGCGC GATTATGCCC TCTTGATCAA CGAATGGCAC CTATTAGCAC GCGCAGTCTT	360
TGTCCTCGAT ACTGACAATA CGATTGCGTA CGTTGAATAC GTGGATAATA TCAATTCTGA	420
GCCAAACTTC GAA	433



## (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:



Phe Thr Gly Lys Gln Leu Gln Val Gly Asp Lys Ala Leu Asp Phe Ser  
 1 5 10 15  
 Leu Thr Thr Thr Asp Leu Ser Lys Lys Ser Leu Ala Asp Phe Asp Gly  
 20 25 30  
 Lys Lys Lys Val Leu Ser Val Val Pro Ser Ile Asp Thr Gly Ile Cys  
 35 40 45  
 Ser Thr Gln Thr Arg Arg Phe Asn Glu Glu Leu Ala Gly Leu Asp Asn  
 50 55 60  
 Thr Val Val Leu Thr Val Ser Met Asp Leu Pro Phe Ala Gln Lys Arg  
 65 70 75 80  
 Trp Cys Gly Ala Glu Gly Leu Asp Asn Ala Ile Met Leu Ser Asp Tyr  
 85 90 95  
 Phe Asp His Ser Phe Gly Arg Asp Tyr Ala Leu Leu Ile Asn Glu Trp  
 100 105 110  
 His Leu Leu Ala Arg Ala Val Phe Val Leu Asp Thr Asp Asn Thr Ile  
 115 120 125  
 Arg Tyr Val Glu Tyr Val Asp Asn Ile Asn Ser Glu Pro Asn Phe Glu  
 130 135 140

## (2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 724 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CCAGGCTGAT ACAAGTATCG CAGACATTCA AAAAAGAGGC GAACTGGTTG TCGGTGTCAA 60  
 ACAAGACGTT CCCAATTTTG GTTACAAnGA TCCAAGACC GGTACTTATT CTGGTATCGA 120  
 AaCCGACTTG GCCAAGATGG TAGCTGATGA ACTCAAGGTC AAGATTCGCT ATGTGCCGGT 180  
 TACAGCACAA ACCCGCGGCC CCCTTCTAGA CAATGAACAG GTCGATATGG ATATCGCGAC 240  
 CTTTACCATC ACGGACGAAC GCAAAAACT CTACAACTTT ACCAGTCCCT ACTACACAGA 300  
 CGCTTCTGGA TTTTGGTCA ATAAATCTGC CAAATCAAA AAGATTGAGG ACCTAAACGG 360

CAAAACCATC GGAGTCGCCC AAGGTTCTAT CACCCAACGC CTGATTACTG AACTGGGTAA 420  
 AAAGAAAGGT CTGAAGTTTA AATTCGTCGA ACTTG GTTCC TACCCAGAAT TGATTACTTC 480  
 CCTGCACGCT CATCGTATCG ATACCTTTTC CGTTGACCGC TCTATTCTAT CTGGCTACAC 540  
 TAGTAAACGG ACAGCACTAC TAGATGATAG TTTCAAGCCA TCTGACTACG GTATTGTTAC 600  
 CAAGAAATCA AATACAGAGC TCAACGACTA TCTTGATAAC TTGGTTACTA AATGGAGCAA 660  
 GGATGGTAGT TTGCAGAAAC TTTATGACCG TTACAAGCTC AAACCATCTA GCCATACTGC 720  
 AGAT 724

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gln Ala Asp Thr Ser Ile Ala Asp Ile Gln Lys Arg Gly Glu Leu Val  
 1 5 10 15  
 Val Gly Val Lys Gln Asp Val Pro Asn Phe Gly Tyr Xaa Asp Pro Lys  
 20 25 30  
 Thr Gly Thr Tyr Ser Gly Ile Glu Thr Asp Leu Ala Lys Met Val Ala  
 35 40 45  
 Asp Glu Leu Lys Val Lys Ile Arg Tyr Val Pro Val Thr Ala Gln Thr  
 50 55 60  
 Arg Gly Pro Leu Leu Asp Asn Glu Gln Val Asp Met Asp Ile Ala Thr  
 65 70 75 80  
 Phe Thr Ile Thr Asp Glu Arg Lys Lys Leu Tyr Asn Phe Thr Ser Pro  
 85 90 95  
 Tyr Tyr Thr Asp Ala Ser Gly Phe Leu Val Asn Lys Ser Ala Lys Ile  
 100 105 110  
 Lys Lys Ile Glu Asp Leu Asn Gly Lys Thr Ile Gly Val Ala Gln Gly  
 115 120 125  
 Ser Ile Thr Gln Arg Leu Ile Thr Glu Leu Gly Lys Lys Lys Gly Leu  
 130 135 140  
 Lys Phe Lys Phe Val Glu Leu Gly Ser Tyr Pro Glu Leu Ile Thr Ser  
 145 150 155 160  
 Leu His Ala His Arg Ile Asp Thr Phe Ser Val Asp Arg Ser Ile Leu  
 165 170 175  
 Ser Gly Tyr Thr Ser Lys Arg Thr Ala Leu Leu Asp Asp Ser Phe Lys  
 180 185 190  
 Pro Ser Asp Tyr Gly Ile Val Thr Lys Lys Ser Asn Thr Glu Leu Asn


195	200	205
Asp Tyr Leu Asp Asn Leu Val Thr Lys Trp Ser Lys Asp Gly Ser Leu		
210	215	220
Gln Lys Leu Tyr Asp Arg Tyr Lys Leu Lys Pro Ser Ser His Thr Ala		
225	230	235
240		
Asp		

## (2) INFORMATION FOR SEQ ID NO: 47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:



GTCTGTATCA TTTGAAAACA AAGAAACAAA CCGTGGTGTC TTgACTTTCA CTATCTCTCA	60
AGACCAAATC AAACCAGAAT TGGACCGTGT CTTCAAGtCA GTGAAGAAAT CTCTTAATGT	120
TCCAGGTTTC CGTAAAGGTC ACCTTCCACG CCCTATCTTC GACCAAAAAT TTGGTGAAGA	180
AGCTCTTTAT CAAGATGCAA TGAACGCACT TTTGCCAAAC GCTTATGAAG CAGCTGTAA	240
AGAAGCTGGT CTTGAAGTGG TTGCCCAACC AAAAATTGAC GTAAC TTCAA TGGAAAAAGG	300
TCAAGACTGG GTTATCACTG CTGAAGTCGT TACAAAACCT GAAGTAAAAT TGGGTGACTA	360
CAAAAACCTT GAAGTATCAG TTGATGTAGA AAAAGAAGTA ACTGACGCTG ATGTCGAAGA	420
GCGTATCGAA CGCGAACGCA ACAACCTGGC TGAATTGGTT ATCAAGGAAG CTGCTGCTGA	480
AAACGGCGAC ACTGTTGTGA TCGACTTCGT TGGTTCATC GACGGTGTG AATTTGACGG	540
TGGAAAAGGT GAAAAC TTCT CACTTG GACT TGGTTCAGGT CAATTCATCC CTGGTTTCGA	600
AGACCAATTG GTAGGTCCT CAGCTGGCGA AACC GTTGAT GTTATCGTAA CATTC CCAGA	660
AGACTACCAA GCAGAAGACC TTGCAGGTAA AGAAGCTAAA TTCGTGACAA CTATCCACGA	720
AGTAAAAGCT AAAGAAGTTC CGGCTCTTGA CGATGAACTT GCAAAAAGACA TTGATGAAGA	780
AGTTGAAACA CTTGCTGACT TGAAAGAAAA ATACAGCAAA GAATTGGCTG CTGCTAAAGA	840
AGAAGCTTAC AAAGATGCAG TTGAAGGTGC AGCAATTGAT ACAGCTGTAG AAAATGCTGA	900
AATCGTAGAA CTTCCAGAAG AAATGATCCA TGAAGAAGTT CACCGTTCAG TAAATGAATT	960
CCTTGGGAAT TTGCAACGTC AAGGGATCAA CCCTGACATG TACTTCCAAA TCACTGGAAC	1020
TACTCAAGAA GACCTTCACA ACCAATACCA AGCAGAAGCT GAGTCACGTA CTAAGACTAA	1080
CCTTGTTATC GAAGCAGTTG CCAAAGCTGA AGGATTTGAT GCTTCAGAAAG AAGAAATCCA	1140
AAAAGAAGTT GAGCAATTGG CAGCAGACTA CAACATGGAA GTTG CACAAG TTCAAACTT	1200
GCTTTCAGCT GACATGTTGA AACATGATAT CACTATCAAA AAAGCTGTTG AATTGATCAC	1260

AAGCACAGCA ACAGTAAAA

1279


## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:



Ser Val Ser Phe Glu Asn Lys Glu Thr Asn Arg Gly Val Leu Thr Phe  
 1 5 10 15  
 Thr Ile Ser Gln Asp Gln Ile Lys Pro Glu Leu Asp Arg Val Phe Lys  
 20 25 30  
 Ser Val Lys Lys Ser Leu Asn Val Pro Gly Phe Arg Lys Gly His Leu  
 35 40 45  
 Pro Arg Pro Ile Phe Asp Gln Lys Phe Gly Glu Glu Ala Leu Tyr Gln  
 50 55 60  
 Asp Ala Met Asn Ala Leu Leu Pro Asn Ala Tyr Glu Ala Ala Val Lys  
 65 70 75 80  
 Glu Ala Gly Leu Glu Val Val Ala Gln Pro Lys Ile Asp Val Thr Ser  
 85 90 95  
 Met Glu Lys Gly Gln Asp Trp Val Ile Thr Ala Glu Val Val Thr Lys  
 100 105 110  
 Pro Glu Val Lys Leu Gly Asp Tyr Lys Asn Leu Glu Val Ser Val Asp  
 115 120 125  
 Val Glu Lys Glu Val Thr Asp Ala Asp Val Glu Glu Arg Ile Glu Arg  
 130 135 140  
 Glu Arg Asn Asn Leu Ala Glu Leu Val Ile Lys Glu Ala Ala Ala Glu  
 145 150 155 160  
 Asn Gly Asp Thr Val Val Ile Asp Phe Val Gly Ser Ile Asp Gly Val  
 165 170 175  
 Glu Phe Asp Gly Gly Lys Gly Glu Asn Phe Ser Leu Gly Leu Gly Ser  
 180 185 190  
 Gly Gln Phe Ile Pro Gly Phe Glu Asp Gln Leu Val Gly His Ser Ala  
 195 200 205  
 Gly Glu Thr Val Asp Val Ile Val Thr Phe Pro Glu Asp Tyr Gln Ala  
 210 215 220  
 Glu Asp Leu Ala Gly Lys Glu Ala Lys Phe Val Thr Thr Ile His Glu  
 225 230 235 240  
 Val Lys Ala Lys Glu Val Pro Ala Leu Asp Asp Glu Leu Ala Lys Asp  
 245 250 255

Ile Asp Glu Glu Val Glu Thr Leu Ala Asp Leu Lys Glu Lys Tyr Ser  
 260 265 270

Lys Glu Leu Ala Ala Ala Lys Glu Glu Ala Tyr Lys Asp Ala Val Glu  
 275 280 285

Gly Ala Ala Ile Asp Thr Ala Val Glu Asn Ala Glu Ile Val Glu Leu  
 290 295 300

Pro Glu Glu Met Ile His Glu Glu Val His Arg Ser Val Asn Glu Phe  
 305 310 315 320

Leu Gly Asn Leu Gln Arg Gln Gly Ile Asn Pro Asp Met Tyr Phe Gln  
 325 330 335

Ile Thr Gly Thr Thr Gln Glu Asp Leu His Asn Gln Tyr Gln Ala Glu  
 340 345 350

Ala Glu Ser Arg Thr Lys Thr Asn Leu Val Ile Glu Ala Val Ala Lys  
 355 360 365

Ala Glu Gly Phe Asp Ala Ser Glu Glu Glu Ile Gln Lys Glu Val Glu  
 370 375 380

Gln Leu Ala Ala Asp Tyr Asn Met Glu Val Ala Gln Val Gln Asn Leu  
 385 390 395 400

Leu Ser Ala Asp Met Leu Lys His Asp Ile Thr Ile Lys Lys Ala Val  
 405 410 415

Glu Leu Ile Thr Ser Thr Ala Thr Val Lys  
 420 425

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 490 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

TGGTCAAAAG GAAAGTCAGA CAGGAAAGGG GATGAAAATT GTGACCAGTT TTTATCCTAT	60
CTACGCTATG GTTAAGGAAG TATCTGGTGA CTTGAATGAT GTTCGGATGA TTCAGTCAAG	120
TAGTGGTATT CACTCCTTTG AACCTTCGGC AAATGATATC GCAGCCATCT ATGATGCAGA	180
TGTCTTTGTT TACCATTCTC ATACACTCGA ATCTTGGGCA GGAAGTCTGG ATCCAAATCT	240
AAAAAATCC AAAGTGAAGG TCTTAGAGGC TTCTGAGGGA ATGACCTTGG AACGTGTCCC	300
TGGACTAGAG GATGTGGAAG CAGGGGATGG AGTTGATGAA AAAACGCTCT ATGACCCTCA	360
CACATGGCTA GATCCTGAAA AAGCTGGAGA AGAAGCCCAA ATTATCGCTG ATAAACTTTC	420
AGAGGTGGAT AGTGAGCATA AAGAGACTTA TCAAAAAAAT GCGCAACCTT TATCAAAAAA	480
GCTCAGGAAT	490

(2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gly Gln Lys Glu Ser Gln Thr Gly Lys Gly Met Lys Ile Val Thr Ser  
 1 5 10 15  
 Phe Tyr Pro Ile Tyr Ala Met Val Lys Glu Val Ser Gly Asp Leu Asn  
 20 25 30  
 Asp Val Arg Met Ile Gln Ser Ser Ser Gly Ile His Ser Phe Glu Pro  
 35 40 45  
 Ser Ala Asn Asp Ile Ala Ala Ile Tyr Asp Ala Asp Val Phe Val Tyr  
 50 55 60  
 His Ser His Thr Leu Glu Ser Trp Ala Gly Ser Leu Asp Pro Asn Leu  
 65 70 75 80  
 Lys Lys Ser Lys Val Lys Val Leu Glu Ala Ser Glu Gly Met Thr Leu  
 85 90 95  
 Glu Arg Val Pro Gly Leu Glu Asp Val Glu Ala Gly Asp Gly Val Asp  
 100 105 110  
 Glu Lys Thr Leu Tyr Asp Pro His Thr Trp Leu Asp Pro Glu Lys Ala  
 115 120 125  
 Gly Glu Glu Ala Gln Ile Ile Ala Asp Lys Leu Ser Glu Val Asp Ser  
 130 135 140  
 Glu His Lys Glu Thr Tyr Gln Lys Asn Ala Gln Pro Leu Ser Lys Lys  
 145 150 155 160  
 Leu Arg Asn

## (2) INFORMATION FOR SEQ ID NO: 51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1006 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAAGGATAGA TATATTTTAG CATTTGAGAC ATCCTGTGAT GAGACCAGTG TCGCCGTCTT 60  
 GAAAAACGAC GATGAGCTCT TGTCCAATGT CATTGCTAGT CAAATTGAGA GTCACAAACG 120  
 TTTTGGTGCC GTAGTGCCCG AAGTAGCCAG TCGTCACCAT GTCGAGGTCA TTACAGCCTG 180  
 TATCGAGGAG GCATTGGCAG AAGCAGGGAT TACCGAAGAG GACGTGACAG CTGTTGCGGT 240

TACCTACGGA CCAGGCTTGG TCGGAGCCTT GCTAGTTGGT TTGTCAGCTG CCAAGGCCTT 300  
 TGCTTGGGCT CACGGACTTC CACTGATTCC TGTTAATCAC ATGGCTGGGC ACCTCATGGC 360  
 AGCTCAGAGT GTGGAGCCTT TGGAGTTTCC CTTGCTAGCC CTCTTGGTCA GCGGCGGACA 420  
 CACAGAGTTG GTTTATGTTT CGGAGGCAGG AGATTATAAG ATTGTTGGGG AAACCCGTGA 480  
 TGATGCGGTT GGTGAGGCTT ATGATAAGGT CGGCCGTGTC ATGGGCTTGA CCTATCCTGC 540  
 AGGTCGTGAG ATTGACGAGC TGGCTCATCA GGGGCAGGAT ATTTATGATT TCCCCCGTGC 600  
 CATGATTAAG GAAGATAATC TGGAGTTCTC CTTCTCAGGT TTGAAATCTG CCTTTATCAA 660  
 TCTTCATCAC AATGCCGAGC AAAAGGGAGA AAGCCTGTCT ACAGAAGATT TGTGTGCTTC 720  
 CTTCCAAGCA GCAGTTATGG ACATTCTCAT GGCAAAAACC AAGAAGGCTT TGGAGAAATA 780  
 TCCTGTAAA ATCCTAGTTG TGGCAGGTGG TGTGGCAGCC AATAAAGGTC TCAGAGAACG 840  
 CCTAGCAGCC GAAATCACAG ATGTCAAGGT TATCATCCCC CCTCTGCGAC TCTGCGGAGA 900  
 CAATGCAGGT ATGATTGCCT ATGCCAGCGT CAGCNAGTGG AACAAAGAAA ACTTCGCAGG 960  
 CTGGGACCTC AATGCCAAAC CAAGTCTTGC CTTTGATACC ATGGAA 1006

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Lys Asp Arg Tyr Ile Leu Ala Phe Glu Thr Ser Cys Asp Glu Thr Ser  
 1 5 10 15  
 Val Ala Val Leu Lys Asn Asp Asp Glu Leu Leu Ser Asn Val Ile Ala  
 20 25 30  
 Ser Gln Ile Glu Ser His Lys Arg Phe Gly Gly Val Val Pro Glu Val  
 35 40 45  
 Ala Ser Arg His His Val Glu Val Ile Thr Ala Cys Ile Glu Glu Ala  
 50 55 60  
 Leu Ala Glu Ala Gly Ile Thr Glu Glu Asp Val Thr Ala Val Ala Val  
 65 70 75 80  
 Thr Tyr Gly Pro Gly Leu Val Gly Ala Leu Leu Val Gly Leu Ser Ala  
 85 90 95  
 Ala Lys Ala Phe Ala Trp Ala His Gly Leu Pro Leu Ile Pro Val Asn  
 100 105 110  
 His Met Ala Gly His Leu Met Ala Ala Gln Ser Val Glu Pro Leu Glu  
 115 120 125

Phe Pro Leu Leu Ala Leu Leu Val Ser Gly Gly His Thr Glu Leu Val  
 130 135 140  
 Tyr Val Ser Glu Ala Gly Asp Tyr Lys Ile Val Gly Glu Thr Arg Asp  
 145 150 155 160  
 Asp Ala Val Gly Glu Ala Tyr Asp Lys Val Gly Arg Val Met Gly Leu  
 165 170 175  
 Thr Tyr Pro Ala Gly Arg Glu Ile Asp Glu Leu Ala His Gln Gly Gln  
 180 185 190  
 Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile Lys Glu Asp Asn Leu Glu  
 195 200 205  
 Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe Ile Asn Leu His His Asn  
 210 215 220  
 Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr Glu Asp Leu Cys Ala Ser  
 225 230 235 240  
 Phe Gln Ala Ala Val Met Asp Ile Leu Met Ala Lys Thr Lys Lys Ala  
 245 250 255  
 Leu Glu Lys Tyr Pro Val Lys Ile Leu Val Val Ala Gly Gly Val Ala  
 260 265 270  
 Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala Ala Glu Ile Thr Asp Val  
 275 280 285  
 Lys Val Ile Ile Pro Pro Leu Arg Leu Cys Gly Asp Asn Ala Gly Met  
 290 295 300  
 Ile Ala Tyr Ala Ser Val Ser Xaa Trp Asn Lys Glu Asn Phe Ala Gly  
 305 310 315 320  
 Trp Asp Leu Asn Ala Lys Pro Ser Leu Ala Phe Asp Thr Met Glu  
 325 330 335

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGTAGTTAAA GTTGGTATTA ACGGTTTCGG ACGTATCGGT CGTCTTGCTT TCCGTCGTAT	60
CCAAAACGTA GAAGGTGTTG AAGTTACACG CATCAACGAC CTTACAGATC CAGTTATGCT	120
TGCACACTTG TTGAAATACG ACACAACCTCA AGGTCGTTTC GACGGTACTG TTGAAGTTAA	180
AGAAGGTGGA TTTGAAGTTA ACGGTAAATT CATCAAAGTT TCTGCTGAAC GTGATCCAGA	240
ACAAATCGAC TGGGCTACTG ACGGTGTAGA AATCGTTCCTT GAAGCTACTG GTTTCTTTGC	300
TAAGAAAGAA GCAGCTGAAA AACACCTTAA AGGTGGAGCT AAAAAAGTTG TTATCACTGC	360
TCCTGGTGGA AACGACGTTA AAACAGTTGT ATTCAACACT AACCACGACG TTCTTGACGG	420



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TACTGAAACA GTTATCTCAG GTGCTTCATG TACTACAAAC TGCTTGGCTC CAATGGCTAA      480
AGCTCTTCAA GACAACTTTG GTGTTGTTGA AGGATTGATG ACTACTATCC ACGCTTACAC      540
TGGTGACCAA ATGATCCTTG ACGGACCACA CCGTGGTGGT GACCTTCGCC GTGCTCGCGC      600
TGGTGCTGCA AACATCGTTC CTAACCAAC TGGTGCTGCA AAAGCTATCG GTCTTGTAAT      660
CCCAGAAATTG AATGGTAAAC TTGACGGATC TGCACAACGC GTTCCAACCTC CAACTGGATC      720
AGTTACTGAA TTGGTAGCAG TTCTTGAAAA GAACGTTACT GTTGATGAAG TGAACGCAGC      780
TATGAAAGCA GCTTCAAACG AATCATACGG TTACACAGAA GATCCAATCG TATCTTCAGA      840
TATCGTAGGT ATGTCTTACG GTTCATTGTT TGACGCAACT CAACTAAAG TTCTTGACGT      900
TGACGGTAAA CAATTGGTTA AAGTTGTATC ATGGTACGAC AACGAAATGT CATACACTGC      960
ACAACTTGTT CGTACTCTTG GAATACTTCG CAAAAATTGC      1000

```


## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:



```

Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Ala
1          5          10
Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile Asn
20        25        30
Asp Leu Thr Asp Pro Val Met Leu Ala His Leu Leu Lys Tyr Asp Thr
35        40        45
Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly Phe
50        55        60
Glu Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Arg Asp Pro Glu
65        70        75        80
Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala Thr
85        90        95
Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu Lys Gly Gly
100       105       110
Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val Lys Thr
115       120       125
Val Val Phe Asn Thr Asn His Asp Val Leu Asp Gly Thr Glu Thr Val
130       135       140
Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys
145       150       155       160

```

Ala Leu Gln Asp Asn Phe Gly Val Val Glu Gly Leu Met Thr Thr Ile  
165 170 175

His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His Arg Gly  
180 185 190

Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val Pro Asn  
195 200 205

Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu Leu Asn  
210 215 220

Gly Lys Leu Asp Gly Ser Ala Gln Arg Val Pro Thr Pro Thr Gly Ser  
225 230 235 240

Val Thr Glu Leu Val Ala Val Leu Glu Lys Asn Val Thr Val Asp Glu  
245 250 255

Val Asn Ala Ala Met Lys Ala Ala Ser Asn Glu Ser Tyr Gly Tyr Thr  
260 265 270

Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Tyr Gly Ser  
275 280 285

Leu Phe Asp Ala Thr Gln Thr Lys Val Leu Asp Val Asp Gly Lys Gln  
290 295 300

Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr Thr Ala  
305 310 315 320

Gln Leu Val Arg Thr Leu Gly Ile Leu Arg Lys Asn Cys  
325 330

## (2) INFORMATION FOR SEQ ID NO: 55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2389 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TTCTTACGAG TTGGGACTGT ATCAAGCTAG AACGGTTAAG GAAAATAATC GTGTTTCCTA 60

TATAGATGGA AAACAAGCGA CGCAAAAAAC GGAGAATTTG ACTCCTGATG AGGTTAGCAA 120

GCGTGAAGGA ATCAATGCTG AGCAAATCGT CATCAAGATA ACAGACCAAG GCTATGTCAC 180

TTCACATGGC GACCACTATC ATTATTACAA TGGTAAGGTT CCTTATGACG CTATCATCAG 240

TGAAGAATTA CTCATGAAAG ATCCAAACTA TAAGCTAAAA GATGAGGATA TTGTTAATGA 300

GGTCAAGGGT GGATATGTTA TCAAGGTAGA TGGAAAATAC TATGTTTACC TTAAGGATGC 360

TGCCCACGCG GATAACGTCC GTACAAAAGA GGAAATCAAT CGACAAAAAC AAGAGCATAG 420

TCAACATCGT GAAGGTGGAA CTCCAAGAAA CGATGGTGCT GTTGCCTTGG CACGTTTCGA 480

AGGACGCTAT ACTACAGATG ATGGTTATAT CTTTAATGCT TCTGATATCA TAGAGGATAC 540

TGGTGATGCT TATATCGTTC CTCATGGAGA TCATTACCAT TACATTCCTA AGAATGAGTT 600

ATCAGCTAGC GAGTTGGCTG CTGCAGAAGC CTTCCATCTT GGTGAGGAA ATCTGTCAAA 660

TTCAAGAACC TATCGCCGAC AAAATAGCGA TAACACTTCA AGAACAAACT GGGTACCTTC 720  
 TGTAAGCAAT CCAGGAAC TA CAAATACTAA CACAAGCAAC AACAGCAACA CTAACAGTCA 780  
 AGCAAGTCAA AGTAATGACA TTGATAGTCT CTTGAAACAG CTCTACAAAC TGCCTTTGAG 840  
 TCAACGACAT GTAGAATCTG ATGGCCTTGT CTTTGATCCA GCACAAATCA CAAGTCGAAC 900  
 AGCTAGAGGT GTTGCAGTGC CACACGGAGA TCATTACCAC TTCATCCCTT ACTCTCAAAT 960  
 GTCTGAATTG GAAGAACGAA TCGCTCGTAT TATTCCCCTT CGTTATCGTT CAAACCATTG 1020  
 GGTACCAGAT TCAAGGCCAG AACAACCAAG TCCACAACCG ACTCCGGAAC CTAGTCCAGG 1080  
 CCCGCAACCT GCACCAAATC TTAAAATAGA CTCAAATTC TCTTTGGTTA GTCAGCTGGT 1140  
 ACGAAAAGTT GGGGAAGGAT ATGTATTCTGA AGAAAAGGGC ATCTCTCGTT ATGTCTTTGC 1200  
 GAAAGATTTA CCATCTGAAA CTGTTAAAAA TCTTGAAAGC AAGTTATCAA AACAAGAGAG 1260  
 TGTTTCACAC ACTTTAACTG CTAAAAAGA AAATGTTGCT CCTCGTGACC AAGAATTTTA 1320  
 TGATAAAGCA TATAATCTGT TAACTGAGGC TCATAAAGCC TTGTTTGNAATAAAGGGTCG 1380  
 TAATTC TGAT TTCCAAGCCT TAGACAAATT ATTAGAACGC TTGAATGATG AATCGACTAA 1440  
 TAAAGAAAAA TTGGTAGATG ATTTATTTGGC ATTCCTAGCA CCAATTACCC ATCCAGAGCG 1500  
 ACTTGGCAAA CCAAATTCCT AAATTGAGTA TACTGAAGAC GAAGTTCGTA TTGCTCAATT 1560  
 AGCTGATAAG TATACAACGT CAGATGGTTA CATTTTTGAT GAACATGATA TAATCAGTGA 1620  
 TGAAGGAGAT GCATATGTAA CGCCTCATAT GGGCCATAGT CACTGGATTG GAAAAGATAG 1680  
 CCTTTCTGAT AAGGAAAAAG TTGCAGCTCA AGCCTATACT AAAGAAAAAG GTATCCTACC 1740  
 TCCATCTCCA GACGCAGATG TTAAAGCAAA TCCAAC TGGA GATAGTGCAG CAGCTATTTA 1800  
 CAATCGTGTG AAAGGGGAAA AACGAATTCC ACTCGTTCGA CTTCCATATA TGGTTGAGCA 1860  
 TACAGTTGAG GTTAAAAACG GTAATTTGAT TATTCCTCAT AAGGATCAT ACCATAATAT 1920  
 TAAATTTGCT TGGTTTGATG ATCACACATA CAAAGCTCCA AATGGCTATA CCTTGAAGA 1980  
 TTTGTTTGCG ACGATTAAGT ACTACGTAGA ACACCTGAC GAACGTCCAC ATTCTAATGA 2040  
 TGGATGGGGC AATGCCAGTG AGCATGTGTT AGGCAAGAAA GACCACAGTG AAGATCCAAA 2100  
 TAAGAACTTC AAAGCGGATG AAGAGCCAGT AGAGGAAACA CCTGCTGAGC CAGAAGTCCC 2160  
 TCAAGTAGAG ACTGAAAAAG TAGAAGCCCA ACTCAAAGAA GCAGAAGTTT TGCTTGCGAA 2220  
 AGTAACGGAT TCTAGTCTGA AAGCCAATGC AACAGAACT CTAGCTGGTT TACGAAATAA 2280  
 TTTGACTCTT CAAATTATGG ATAACAATAG TATCATGGCA GAAGCAGAAA AATTACTTGC 2340  
 GTTGTTAAAA GGAAGTAATC CTTCATCTGT AAGTAAGGAA AAAATAAAC 2389

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 796 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Tyr Glu Leu Gly Leu Tyr Gln Ala Arg Thr Val Lys Glu Asn Asn  
1 5 10 15  
Arg Val Ser Tyr Ile Asp Gly Lys Gln Ala Thr Gln Lys Thr Glu Asn  
20 25 30  
Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala Glu Gln  
35 40 45  
Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp  
50 55 60  
His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile Ile Ser  
65 70 75 80  
Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Lys Leu Lys Asp Glu Asp  
85 90 95  
Ile Val Asn Glu Val Lys Gly Gly Tyr Val Ile Lys Val Asp Gly Lys  
100 105 110  
Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr  
115 120 125  
Lys Glu Glu Ile Asn Arg Gln Lys Gln Glu His Ser Gln His Arg Glu  
130 135 140  
Gly Gly Thr Pro Arg Asn Asp Gly Ala Val Ala Leu Ala Arg Ser Gln  
145 150 155 160  
Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile  
165 170 175  
Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His Tyr  
180 185 190  
His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala Ala  
195 200 205  
Glu Ala Phe Leu Ser Gly Arg Gly Asn Leu Ser Asn Ser Arg Thr Tyr  
210 215 220  
Arg Arg Gln Asn Ser Asp Asn Thr Ser Arg Thr Asn Trp Val Pro Ser  
225 230 235 240  
Val Ser Asn Pro Gly Thr Thr Asn Thr Asn Thr Ser Asn Asn Ser Asn  
245 250 255  
Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp Ile Asp Ser Leu Leu Lys  
260 265 270  
Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val Glu Ser Asp Gly  
275 280 285  
Leu Val Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala Arg Gly Val  
290 295 300

Ala Val Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Gln Met  
 305 310 315 320  
 Ser Glu Leu Glu Glu Arg Ile Ala Arg Ile Ile Pro Leu Arg Tyr Arg  
 325 330 335  
 Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln Pro Ser Pro Gln  
 340 345 350  
 Pro Thr Pro Glu Pro Ser Pro Gly Pro Gln Pro Ala Pro Asn Leu Lys  
 355 360 365  
 Ile Asp Ser Asn Ser Ser Leu Val Ser Gln Leu Val Arg Lys Val Gly  
 370 375 380  
 Glu Gly Tyr Val Phe Glu Glu Lys Gly Ile Ser Arg Tyr Val Phe Ala  
 385 390 395 400  
 Lys Asp Leu Pro Ser Glu Thr Val Lys Asn Leu Glu Ser Lys Leu Ser  
 405 410 415  
 Lys Gln Glu Ser Val Ser His Thr Leu Thr Ala Lys Lys Glu Asn Val  
 420 425 430  
 Ala Pro Arg Asp Gln Glu Phe Tyr Asp Lys Ala Tyr Asn Leu Leu Thr  
 435 440 445  
 Glu Ala His Lys Ala Leu Phe Xaa Asn Lys Gly Arg Asn Ser Asp Phe  
 450 455 460  
 Gln Ala Leu Asp Lys Leu Leu Glu Arg Leu Asn Asp Glu Ser Thr Asn  
 465 470 475 480  
 Lys Glu Lys Leu Val Asp Asp Leu Leu Ala Phe Leu Ala Pro Ile Thr  
 485 490 495  
 His Pro Glu Arg Leu Gly Lys Pro Asn Ser Gln Ile Glu Tyr Thr Glu  
 500 505 510  
 Asp Glu Val Arg Ile Ala Gln Leu Ala Asp Lys Tyr Thr Thr Ser Asp  
 515 520 525  
 Gly Tyr Ile Phe Asp Glu His Asp Ile Ile Ser Asp Glu Gly Asp Ala  
 530 535 540  
 Tyr Val Thr Pro His Met Gly His Ser His Trp Ile Gly Lys Asp Ser  
 545 550 555 560  
 Leu Ser Asp Lys Glu Lys Val Ala Ala Gln Ala Tyr Thr Lys Glu Lys  
 565 570 575  
 Gly Ile Leu Pro Pro Ser Pro Asp Ala Asp Val Lys Ala Asn Pro Thr  
 580 585 590  
 Gly Asp Ser Ala Ala Ala Ile Tyr Asn Arg Val Lys Gly Glu Lys Arg  
 595 600 605  
 Ile Pro Leu Val Arg Leu Pro Tyr Met Val Glu His Thr Val Glu Val  
 610 615 620  
 Lys Asn Gly Asn Leu Ile Ile Pro His Lys Asp His Tyr His Asn Ile  
 625 630 635 640

Lys Phe Ala Trp Phe Asp Asp His Thr Tyr Lys Ala Pro Asn Gly Tyr  
 645 650 655  
 Thr Leu Glu Asp Leu Phe Ala Thr Ile Lys Tyr Tyr Val Glu His Pro  
 660 665 670  
 Asp Glu Arg Pro His Ser Asn Asp Gly Trp Gly Asn Ala Ser Glu His  
 675 680 685  
 Val Leu Gly Lys Lys Asp His Ser Glu Asp Pro Asn Lys Asn Phe Lys  
 690 695 700  
 Ala Asp Glu Glu Pro Val Glu Glu Thr Pro Ala Glu Pro Glu Val Pro  
 705 710 715 720  
 Gln Val Glu Thr Glu Lys Val Glu Ala Gln Leu Lys Glu Ala Glu Val  
 725 730 735  
 Leu Leu Ala Lys Val Thr Asp Ser Ser Leu Lys Ala Asn Ala Thr Glu  
 740 745 750  
 Thr Leu Ala Gly Leu Arg Asn Asn Leu Thr Leu Gln Ile Met Asp Asn  
 755 760 765  
 Asn Ser Ile Met Ala Glu Ala Glu Lys Leu Leu Ala Leu Leu Lys Gly  
 770 775 780  
 Ser Asn Pro Ser Ser Val Ser Lys Glu Lys Ile Asn  
 785 790 795

## (2) INFORMATION FOR SEQ ID NO: 57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TACTGAGATG CATCATAATC TAGGAGCTGA AAAGCGTTCA GCAGTGGCTA CTACTATCGA 60  
 TAGTTTTAAG GAGCGAAGTC AAAAAGTCAG AGCACTATCT GATCCAAATG TCGGTTTTGT 120  
 TCCCTTCTTT GGCTCTAGTG AATGGCTTCG TTTTGACGGT GCTCATTCTG CGGTATTAGC 180  
 TGAGAAATAC AATCGTTCCT ACCGTCCTTA TCTTTTAGGA CAGGGGGGAG CTGCATCGCT 240  
 TAACCAATAT TTTGGAATGC AACAGATGTT ACCACAGCTG GAGAATAAAC AAGTTGTGTA 300  
 TGTATCTCA CCTCAGTGGT TCAGTAAAAA TGGCTATGAT CCAGCAGCCT TCCAGCAGTA 360  
 TTTTAATGGA GACCAGTTGA CTAGTTTTCT GAAACATCAA TCTGGGGATC AGGCTAGTCA 420  
 ATATGCAGCG ACTCGCTTAC TGCAACAGTT CCCAAACGTA GCTATGAAGG ACCTGGTTCA 480  
 GAAGTTGGCA AGTAAAGAAG AATTGTCGAC AGCAGACAAT GAAATGATTG AATTATTGGC 540  
 TCGTTTTAAT GAACGCCAAG CTTCCTTTTT TGGTCAGTTT TCGGTTAGAG GCTATGTTAA 600  
 CTACGATAAG CATGTAGCTA AGTATTTAAA AATCTTGCCA GACCAGTTTT CTTATCAGGC 660

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AATAGAAGAT GTTGTCAAAG CAGATGCTGA AAAAAATACT TCCAATAATG AGATGGGAAT      720
GGAAAATTAT TTCTATAATG AGCAGATCAA GAAGGATTTG AAGAAATTAA AGGATTCTCA      780
GAAAAGCTTT ACCTATCTCA AGTCGCCAGA GTATAATGNN TTGCAGTTGG TTTTAACACA      840
GTTTTCTAAA TCTAAGGTAA ACCCGATTTT TATCATTTCA CCTGTTAATA AAAAATGGAT      900
GNACTATGCT GGTCTACGAG AGGATATGTA CCAACAAACG GTGCAGAAGA TTCGCTACCA      960
GTTAGAAAGT CAAGGTTTTA CCAATATAGC AGATTTTTCT AAGGACGGCG GGGAGCCTTT      1020
CTTTATGAAG GACACCATTC ACCTTG GTTGGTGG TTGGCTTTTG ACAAGGCAGT      1080
TGATCCTTTC CTATCCAATC CCACACCAGC TCCGACTTAC CATCTGAATG AGCGCTTTTT      1140
CAGCAAAGAT TGGGCGACTT ATGATGGAGA TGTCAAAGAA      1180

```


## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:



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Thr Glu Met His His Asn Leu Gly Ala Glu Lys Arg Ser Ala Val Ala
1          5          10          15
Thr Thr Ile Asp Ser Phe Lys Glu Arg Ser Gln Lys Val Arg Ala Leu
20        25        30
Ser Asp Pro Asn Val Arg Phe Val Pro Phe Phe Gly Ser Ser Glu Trp
35        40        45
Leu Arg Phe Asp Gly Ala His Ser Ala Val Leu Ala Glu Lys Tyr Asn
50        55        60
Arg Ser Tyr Arg Pro Tyr Leu Leu Gly Gln Gly Gly Ala Ala Ser Leu
65        70        75        80
Asn Gln Tyr Phe Gly Met Gln Gln Met Leu Pro Gln Leu Glu Asn Lys
85        90        95
Gln Val Val Tyr Val Ile Ser Pro Gln Trp Phe Ser Lys Asn Gly Tyr
100       105       110
Asp Pro Ala Ala Phe Gln Gln Tyr Phe Asn Gly Asp Gln Leu Thr Ser
115       120       125
Phe Leu Lys His Gln Ser Gly Asp Gln Ala Ser Gln Tyr Ala Ala Thr
130       135       140
Arg Leu Leu Gln Gln Phe Pro Asn Val Ala Met Lys Asp Leu Val Gln
145       150       155       160
Lys Leu Ala Ser Lys Glu Glu Leu Ser Thr Ala Asp Asn Glu Met Ile
165       170       175

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Glu Leu Leu Ala Arg Phe Asn Glu Arg Gln Ala Ser Phe Phe Gly Gln  
 180 185 190  
 Phe Ser Val Arg Gly Tyr Val Asn Tyr Asp Lys His Val Ala Lys Tyr  
 195 200 205  
 Leu Lys Ile Leu Pro Asp Gln Phe Ser Tyr Gln Ala Ile Glu Asp Val  
 210 215 220  
 Val Lys Ala Asp Ala Glu Lys Asn Thr Ser Asn Asn Glu Met Gly Met  
 225 230 235 240  
 Glu Asn Tyr Phe Tyr Asn Glu Gln Ile Lys Lys Asp Leu Lys Lys Leu  
 245 250 255  
 Lys Asp Ser Gln Lys Ser Phe Thr Tyr Leu Lys Ser Pro Glu Tyr Asn  
 260 265 270  
 Xaa Leu Gln Leu Val Leu Thr Gln Phe Ser Lys Ser Lys Val Asn Pro  
 275 280 285  
 Ile Phe Ile Ile Pro Pro Val Asn Lys Lys Trp Met Xaa Tyr Ala Gly  
 290 295 300  
 Leu Arg Glu Asp Met Tyr Gln Gln Thr Val Gln Lys Ile Arg Tyr Gln  
 305 310 315 320  
 Leu Glu Ser Gln Gly Phe Thr Asn Ile Ala Asp Phe Ser Lys Asp Gly  
 325 330 335  
 Gly Glu Pro Phe Phe Met Lys Asp Thr Ile His Leu Gly Trp Leu Gly  
 340 345 350  
 Trp Leu Ala Phe Asp Lys Ala Val Asp Pro Phe Leu Ser Asn Pro Thr  
 355 360 365  
 Pro Ala Pro Thr Tyr His Leu Asn Glu Arg Phe Phe Ser Lys Asp Trp  
 370 375 380  
 Ala Thr Tyr Asp Gly Asp Val Lys Glu  
 385 390

## (2) INFORMATION FOR SEQ ID NO: 59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GGTTTGTGAGA AAGTATTTGC AGGGGGCCCT GATTGAGTCG ATTGAGCAAG TGGAAAATGA	60
CCGTATTGTG GAAATTACAG TTTCCAATAA AAACGAGATT GGAGACCATA TCCAGGCTAC	120
CTTGATTATC GAAATTATGG GGAAACACAG TAATATTCTA CTGGTCGATA AAAGCAGTCA	180
TAAAATCCTC GAAGTTATCA AACACGTCGG CTTTTCACAA AATAGCTACC GCACCTTACT	240
TCCAGGATCG ACCTATATCG CTCCGCCAAG TACAAAATCT CTCAATCCTT TTACTATCAA	300





GGATGAAAAG CTCTTTGAAA TCCTGCAAAC CCAAGAACTA ACAGCAAAAA ATCTTCAAAG	360
CCTCTTTCAA GGTCTGGGAC GCGATACGGC AAATGAATTG GAAAGGATAC TGGTTAGTGA	420
AAAACTTTCC GCTTTCCGAA ATTTTTTTCAA TCAAGAAACC AAGCCATGCT TGACTGAGAC	480
TTCTTTCAGT CCAGTTCCTT TTGCAAATCA GGTGGGAGAG CCTTTTGCAA ATCTTCTGA	540
TTTGTGGAC ACCTACTATA AGGATAAGGC TGAGCGCGAC CGCGTCAAAC AGCAGGCCAG	600
TGAACGTATT CGTCGTGTTG AAAATGAACT TCAGAAAAAC CGACACAAAC TCAAAAAACA	660
GGAAAAAGAG TTACTGGCGA CAGACAACGC TGAAGAATTT CGTCAAAAAG GAGAATTGCT	720
GACAACCTTC CTCCACCAAG TGCCTAACGA CCAAGACCAG GTTATCCTAG ACAACTACTA	780
TACCAACCAA CCTATCATGA TTGCGCTTGA TAAGGCTCTG ACTCCCAACC AGAATGCCCA	840
ACGCTATTTT AAACGGTATC AGAAACTCAA AGAAGCTGTC AAATACCTGA CTGATTTGAT	900
TGAAGAAACC AAAGCCACTA TTCTCTATCT GGAAAGTGTA GAAACCGTCC TCAACCAAGC	960
TGGACTGGAA GAAATCGCTG AAATCCGTGA AGAATTGATT CAAACAGGTT TTATCCGCAG	1020
AAGACAACGG GAGAAAATCC AGAAACGCAA AAAACTAGAA CAATATCTAG CAAGCGATGG	1080
CAAAACCATC ATCTATGTCG GACGAAACAA TCTTCAAAAT GAGGAATTGA CCTTTAAAT	1140
GGCCCGCAAG GAGGAACTTT GGTTCATGC TAAGGACATT CCTGGAAGCC ATGTTGTCAT	1200
CTCAGGAAAT CTTGACCCAT CTGATGCAGT CAAGACAGAC GCAGCAGAGT TAGTCGCCTA	1260
CTTCTCTCAA GGGCGCCTGT CGAATCTGGT GCAGGTAGAT ATGATTGAAG TCAAAAACT	1320
CAATAAACCA ACTGGTGGAA AACCCGGCTT TGTCACCTAC ACAGGACAAA AGACCCTCCG	1380
CGTCACACCA GACTCCAAAA AAATTGCATC CATGAAAAAA TCC	1423

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Val Leu Arg Lys Tyr Leu Gln Gly Ala Leu Ile Glu Ser Ile Glu Gln  
 1 5 10 15

Val Glu Asn Asp Arg Ile Val Glu Ile Thr Val Ser Asn Lys Asn Glu  
 20 25 30

Ile Gly Asp His Ile Gln Ala Thr Leu Ile Ile Glu Ile Met Gly Lys  
 35 40 45

His Ser Asn Ile Leu Leu Val Asp Lys Ser Ser His Lys Ile Leu Glu  
 50 55 60

Val Ile Lys His Val Gly Phe Ser Gln Asn Ser Tyr Arg Thr Leu Leu

65						70						75						80
Pro	Gly	Ser	Thr	Tyr 85	Ile	Ala	Pro	Pro	Ser 90	Thr	Lys	Ser	Leu	Asn 95	Pro			
Phe	Thr	Ile	Lys 100	Asp	Glu	Lys	Leu	Phe 105	Glu	Ile	Leu	Gln	Thr 110	Gln	Glu			
Leu	Thr	Ala 115	Lys	Asn	Leu	Gln	Ser 120	Leu	Phe	Gln	Gly	Leu 125	Gly	Arg	Asp			
Thr	Ala 130	Asn	Glu	Leu	Glu	Arg 135	Ile	Leu	Val	Ser	Glu 140	Lys	Leu	Ser	Ala			
Phe 145	Arg	Asn	Phe	Phe	Asn 150	Gln	Glu	Thr	Lys	Pro 155	Cys	Leu	Thr	Glu	Thr 160			
Ser	Phe	Ser	Pro	Val 165	Pro	Phe	Ala	Asn	Gln 170	Val	Gly	Glu	Pro	Phe 175	Ala			
Asn	Leu	Ser	Asp 180	Leu	Leu	Asp	Thr	Tyr 185	Tyr	Lys	Asp	Lys	Ala 190	Glu	Arg			
Asp	Arg	Val 195	Lys	Gln	Gln	Ala	Ser 200	Glu	Leu	Ile	Arg	Arg 205	Val	Glu	Asn			
Glu	Leu 210	Gln	Lys	Asn	Arg	His 215	Lys	Leu	Lys	Lys	Gln 220	Glu	Lys	Glu	Leu			
Leu 225	Ala	Thr	Asp	Asn	Ala 230	Glu	Glu	Phe	Arg	Gln 235	Lys	Gly	Glu	Leu	Leu 240			
Thr	Thr	Phe	Leu	His 245	Gln	Val	Pro	Asn	Asp 250	Gln	Asp	Gln	Val	Ile 255	Leu			
Asp	Asn	Tyr	Tyr 260	Thr	Asn	Gln	Pro	Ile 265	Met	Ile	Ala	Leu	Asp 270	Lys	Ala			
Leu	Thr	Pro 275	Asn	Gln	Asn	Ala	Gln 280	Arg	Tyr	Phe	Lys	Arg 285	Tyr	Gln	Lys			
Leu	Lys 290	Glu	Ala	Val	Lys	Tyr 295	Leu	Thr	Asp	Leu	Ile 300	Glu	Glu	Thr	Lys			
Ala 305	Thr	Ile	Leu	Tyr	Leu 310	Glu	Ser	Val	Glu	Thr 315	Val	Leu	Asn	Gln	Ala 320			
Gly	Leu	Glu	Glu	Ile 325	Ala	Glu	Ile	Arg	Glu 330	Glu	Leu	Ile	Gln	Thr 335	Gly			
Phe	Ile	Arg	Arg 340	Arg	Gln	Arg	Glu	Lys 345	Ile	Gln	Lys	Arg	Lys 350	Lys	Leu			
Glu	Gln	Tyr 355	Leu	Ala	Ser	Asp	Gly 360	Lys	Thr	Ile	Ile	Tyr 365	Val	Gly	Arg			
Asn	Asn 370	Leu	Gln	Asn	Glu	Glu 375	Leu	Thr	Phe	Lys	Met 380	Ala	Arg	Lys	Glu			
Glu 385	Leu	Trp	Phe	His	Ala 390	Lys	Asp	Ile	Pro	Gly 395	Ser	His	Val	Val	Ile 400			
Ser	Gly	Asn	Leu	Asp 405	Pro	Ser	Asp	Ala	Val 410	Lys	Thr	Asp	Ala	Ala 415	Glu			



(2) INFORMATION FOR SEQ ID NO: 63:

(A) LENGTH: 811 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

GGCTAAGGAA	AGAGTGGATG	TACTAGCTTA	TAAACAGGGG	TTGTTTGAAA	CGAGAGAGCA	60
GGCCAAGCGA	GGTGTGATGG	CTGGCCTAGT	CGTAGCAGTC	CTTAATGGAG	AACGGTTTGA	120
CAAGCCAGGA	GAGAAAATTC	CAGATGACAC	CGAATTAAAA	CTCAAGGGGG	AGAAACTCAA	180
GTATGTCAGC	CGTGGTGGTT	TGAAACTGGA	AAAGGCCTTG	CAGGTCTTTG	ATTTGTCGGT	240
GGATGGCGCG	ACTACGATTG	ATATCGGGGC	CTCTACTGGA	GGTTTTACCG	ATGTCATGCT	300
ACAGAATAGT	GCCAAGTTGG	TCTTTGCAGT	CGATGTTGGT	ACCAATCAGT	TGGCTTGGAA	360
ATTACGCCAA	GACCCACGAG	TTGTCAGCAT	GGAGCAGTTC	AATTTCCGCT	ATGCTGAAAA	420
GACTGATTTC	GAGCAGGAGC	CGAGCTTTGC	CAGTATTGAT	GTGAGTTTCA	TTTCCCTTAG	480
TCTGATTTTG	CCAGCCTTGC	ACCGTGTCTT	GGCTGATCAA	GGTCAGGTGG	TAGCACTTGT	540
CAAACCTCAG	TTTGAGGCAG	GACGTGAGCA	GATTGGGAAA	AATGGAATTA	TTCGAGATGC	600
TAAGGTTTCAT	CAGAATGTCC	TTGAATCTGT	AACAGCTATG	GCAGTAGAGG	TAGGTTTTTC	660

AGTCCTTGGC TTGGACTTTT CTCCCATCCA AGGTGGACAT GGAAATATTG AATTTTTAGC 720  
 GTATTTGAAA AAAGAAAAGT CAGCAAGCAA TCAGATTCTT GCTGAGATTA AAGAAGCAGT 780  
 AGAGAGGGCG CATAGTCAAT TAAAAATGA A 811

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala Lys Glu Arg Val Asp Val Leu Ala Tyr Lys Gln Gly Leu Phe Glu  
 1 5 10 15  
 Thr Arg Glu Gln Ala Lys Arg Gly Val Met Ala Gly Leu Val Val Ala  
 20 25 30  
 Val Leu Asn Gly Glu Arg Phe Asp Lys Pro Gly Glu Lys Ile Pro Asp  
 35 40 45  
 Asp Thr Glu Leu Lys Leu Lys Gly Glu Lys Leu Lys Tyr Val Ser Arg  
 50 55 60  
 Gly Gly Leu Lys Leu Glu Lys Ala Leu Gln Val Phe Asp Leu Ser Val  
 65 70 75 80  
 Asp Gly Ala Thr Thr Ile Asp Ile Gly Ala Ser Thr Gly Gly Phe Thr  
 85 90 95  
 Asp Val Met Leu Gln Asn Ser Ala Lys Leu Val Phe Ala Val Asp Val  
 100 105 110  
 Gly Thr Asn Gln Leu Ala Trp Lys Leu Arg Gln Asp Pro Arg Val Val  
 115 120 125  
 Ser Met Glu Gln Phe Asn Phe Arg Tyr Ala Glu Lys Thr Asp Phe Glu  
 130 135 140  
 Gln Glu Pro Ser Phe Ala Ser Ile Asp Val Ser Phe Ile Ser Leu Ser  
 145 150 155 160  
 Leu Ile Leu Pro Ala Leu His Arg Val Leu Ala Asp Gln Gly Gln Val  
 165 170 175  
 Val Ala Leu Val Lys Pro Gln Phe Glu Ala Gly Arg Glu Gln Ile Gly  
 180 185 190  
 Lys Asn Gly Ile Ile Arg Asp Ala Lys Val His Gln Asn Val Leu Glu  
 195 200 205  
 Ser Val Thr Ala Met Ala Val Glu Val Gly Phe Ser Val Leu Gly Leu  
 210 215 220  
 Asp Phe Ser Pro Ile Gln Gly Gly His Gly Asn Ile Glu Phe Leu Ala  
 225 230 235 240

Tyr Leu Lys Lys Glu Lys Ser Ala Ser Asn Gln Ile Leu Ala Glu Ile  
 245 250 255

Lys Glu Ala Val Glu Arg Ala His Ser Gln Phe Lys Asn Glu  
 260 265 270

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTGTTCCCTAT GAACTTGGTC GTCACCAAGC TGGTCAGGTT AAGAAAGAGT CTAATCGAGT 60  
 TTCTTATATA GATGGTGATC AGGCTGGTCA AAAGGCAGAA AACTTGACAC CAGATGAAGT 120  
 CAGTAAGAGG GAGGGGATCA ACGCCGAACA AATNGTNATC AAGATTACGG ATCAAGGTTA 180  
 TGTGACCTCT CATGGAGACC ATTATCATT AATAATGGC AAGGTTCCCTT ATGATGCCAT 240  
 CATCAGTGAA GAGCTCCTCA TGAAAGATCC GAATTATCAG TTGAAGGATT CAGACATTGT 300  
 CAATGAAATC AAGGGTGGTT ATGTCATTAA GGTAAACGGT AAATACTATG TNTACCTTAA 360  
 GGATGCAGCT CATGCGGATA ATATTCGGAC AAAAGAAGAG ATTAAACGTC AGAAGCAGGA 420  
 ACGCAGTCAT AATCATAACT CAAGAGCAGA TAATGCTGTT GCTGCAGCCA GAGCCCAAGG 480  
 ACGTTATACA ACGGATGATG GGTATATCTT CAATGCATCT GATATCATTG AGGACACGGG 540  
 TGATGCTTAT ATCGTTCCCTC ACGGCGACCA TTACCATTAC ATTCCTAAGA ATGAGTTATC 600  
 AGCTAGCGAG TTAGCTGCTG CAGAAGCCTA TTGGAATGGG AAGCAGGGAT CTCGTCCTTC 660  
 TTCAAGTTCT AGTTATAATG CAAATCCAGC TCAACCAAGA TTGTCAGAGA ACCACAATCT 720  
 GACTGTCACT CCAACTTATC ATCAAAATCA AGGGGAAAAC ATTTCAAGCC TTTTACGTGA 780  
 ATTGTATGCT AAACCCCTTAT CAGAACGCCA TGTGGAATCT GATGGCCTTA TTTTCGACCC 840  
 AGCGCAAATC ACAAGTCGAA CCGCCAGAGG TGTAGCTGTC CCTCATGGTA ACCATTACCA 900  
 CTTTATCCCT TATGAACAAA TGTCTGAATT GGAAAAACGA ATTGCTCGTA TTATTCCTCT 960  
 TCGTTATCGT TCAAACCAT TGGTACCAGA TTCAAGACCA GAACAACCAA GTCCACAATC 1020  
 GACTCCGGAA CCTAGTCCAA GTCCGCAACC TGCACCAAAT CCTCAACCAG CTCCAAGCAA 1080  
 TCCAATTGAT GAGAAATTGG TCAAAGAAGC TGTTTCGAAAA GTAGGCGATG GTTATGTCTT 1140  
 TGAGGAGAAT GGAGTTTCTC GTTATATCCC AGCCAAGGAT CTTTCAGCAG AAACAGCAGC 1200  
 AGGCATTGAT AGCAAATGG CCAAGCAGGA AAGTTTATCT CATAAGCTAG GAGCTAAGAA 1260  
 AACTGACCTC CCATCTAGTG ATCGAGAATT TTACAATAAG GCTTATGACT TACTAGCAAG 1320  
 AATTCACCAA GATTTACTTG ATAATAAAGG TCGACAAGTT GATTTTGAGG CTTTGGATAA 1380

CCTGTTGGAA CGACTCAAGG ATGTCNCAAG TGATAAAGTC AAGTTAGTGG ANGATATTCT 1440  
 TGCCTTCTTA GCTCCGATTC GTCATCCAGA ACGTTTAGGA AAACCAAATG CGCAAATTAC 1500  
 CTACACTGAT GATGAGATTC AAGTAGCCAA GTTGGCAGGC AAGTACACAA CAGAAGACGG 1560  
 TTATATCTTT GATCCTCGTG ATATAACCAG TGATGAGGGG GATGCCATATG TAACTCCACA 1620  
 TATGACCCAT AGCCACTGGA TTAAAAAAGA TAGTTTGTCT GAAGCTGAGA GAGCGGCAGC 1680  
 CCAGGCTTAT GCTAAAGAGA AAGGTTTGAC CCCTCCTTCG ACAGACCATC AGGATTCAGG 1740  
 AAATACTGAG GCAAAAGGAG CAGAAGCTAT CTACAACCGC GTGAAAGCAG CTAAGAAGGT 1800  
 GCCACTTGAT CGTATGCCTT ACAATCTTCA ATATACTGTA GAAGTCAAAA ACGGTAGTTT 1860  
 AATCATACCT CATTATGACC ATTACCATAA CATCAAATTT GAGTGGTTTG ACGAAGGCCT 1920  
 TTATGAGGCA CCTAAGGGGT ATACTCTTGA GGATCTTTTG GCGACTGTCA AGTACTATGT 1980  
 CGAACATCCA AACGAACGTC CGCATTCAGA TAATGGTTTT GGTAACGCTA GCGACCATGT 2040  
 TCAAAGAAAC AAAAATGGTC AAGCTGATAC CAATCAAACG GAAAAACCAA GCGAGGAGAA 2100  
 ACCTCAGACA GAAAAACCTG AGGAAGAAAC CCCTCGAGAA GAGAAACCGC AAAGCGAGAA 2160  
 ACCAGAGTCT CCAAACCAA CAGAGGAACC AGAAGAATCA CCAGAGGAAT CAGAAGAACC 2220  
 TCAGGTCGAG ACTGAAAAGG TTGAAGAAAA ACTGAGAGAG GCTGAAGATT TACTTGGAAA 2280  
 AATCCAGGAT 2290

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu  
 1 5 10 15  
 Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala  
 20 25 30  
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala  
 35 40 45  
 Glu Gln Xaa Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His  
 50 55 60  
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile  
 65 70 75 80  
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp  
 85 90 95  
 Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asn

100							105							110						
Gly	Lys	Tyr	Tyr	Val	Tyr	Leu	Lys	Asp	Ala	Ala	His	Ala	Asp	Asn	Ile					
		115					120					125								
Arg	Thr	Lys	Glu	Glu	Ile	Lys	Arg	Gln	Lys	Gln	Glu	Arg	Ser	His	Asn					
	130					135					140									
His	Asn	Ser	Arg	Ala	Asp	Asn	Ala	Val	Ala	Ala	Ala	Arg	Ala	Gln	Gly					
145					150					155					160					
Arg	Tyr	Thr	Thr	Asp	Asp	Gly	Tyr	Ile	Phe	Asn	Ala	Ser	Asp	Ile	Ile					
				165					170					175						
Glu	Asp	Thr	Gly	Asp	Ala	Tyr	Ile	Val	Pro	His	Gly	Asp	His	Tyr	His					
			180					185					190							
Tyr	Ile	Pro	Lys	Asn	Glu	Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala	Ala	Glu					
		195					200					205								
Ala	Tyr	Trp	Asn	Gly	Lys	Gln	Gly	Ser	Arg	Pro	Ser	Ser	Ser	Ser	Ser					
	210					215					220									
Tyr	Asn	Ala	Asn	Pro	Ala	Gln	Pro	Arg	Leu	Ser	Glu	Asn	His	Asn	Leu					
225					230					235					240					
Thr	Val	Thr	Pro	Thr	Tyr	His	Gln	Asn	Gln	Gly	Glu	Asn	Ile	Ser	Ser					
				245					250					255						
Leu	Leu	Arg	Glu	Leu	Tyr	Ala	Lys	Pro	Leu	Ser	Glu	Arg	His	Val	Glu					
			260					265					270							
Ser	Asp	Gly	Leu	Ile	Phe	Asp	Pro	Ala	Gln	Ile	Thr	Ser	Arg	Thr	Ala					
		275					280					285								
Arg	Gly	Val	Ala	Val	Pro	His	Gly	Asn	His	Tyr	His	Phe	Ile	Pro	Tyr					
	290					295					300									
Glu	Gln	Met	Ser	Glu	Leu	Glu	Lys	Arg	Ile	Ala	Arg	Ile	Ile	Pro	Leu					
305					310					315					320					
Arg	Tyr	Arg	Ser	Asn	His	Trp	Val	Pro	Asp	Ser	Arg	Pro	Glu	Gln	Pro					
				325					330					335						
Ser	Pro	Gln	Ser	Thr	Pro	Glu	Pro	Ser	Pro	Ser	Pro	Gln	Pro	Ala	Pro					
			340					345					350							
Asn	Pro	Gln	Pro	Ala	Pro	Ser	Asn	Pro	Ile	Asp	Glu	Lys	Leu	Val	Lys					
		355						360				365								
Glu	Ala	Val	Arg	Lys	Val	Gly	Asp	Gly	Tyr	Val	Phe	Glu	Glu	Asn	Gly					
	370					375					380									
Val	Ser	Arg	Tyr	Ile	Pro	Ala	Lys	Asp	Leu	Ser	Ala	Glu	Thr	Ala	Ala					
385					390					395					400					
Gly	Ile	Asp	Ser	Lys	Leu	Ala	Lys	Gln	Glu	Ser	Leu	Ser	His	Lys	Leu					
				405					410					415						
Gly	Ala	Lys	Lys	Thr	Asp	Leu	Pro	Ser	Ser	Asp	Arg	Glu	Phe	Tyr	Asn					
			420					425					430							
Lys	Ala	Tyr	Asp	Leu	Leu	Ala	Arg	Ile	His	Gln	Asp	Leu	Leu	Asp	Asn					
		435						440				445								



Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg  
 450 455 460  
 Leu Lys Asp Val Xaa Ser Asp Lys Val Lys Leu Val Xaa Asp Ile Leu  
 465 470 475 480  
 Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn  
 485 490 495  
 Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala  
 500 505 510  
 Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile  
 515 520 525  
 Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser  
 530 535 540  
 His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala  
 545 550 555 560  
 Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His  
 565 570 575  
 Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn  
 580 585 590  
 Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn  
 595 600 605  
 Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His  
 610 615 620  
 Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu  
 625 630 635 640  
 Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val  
 645 650 655  
 Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly  
 660 665 670  
 Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala  
 675 680 685  
 Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu  
 690 695 700  
 Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys  
 705 710 715 720  
 Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Ser Pro Glu Glu  
 725 730 735  
 Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu Arg  
 740 745 750  
 Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp  
 755 760

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

TTATAAGGGT GAATTAGAAA AAGGATACCA ATTTGATGGT TGGGAAATTT CTGGTTTCGA      60
AGGTAAAAAA GACGCTGGCT ATGTTATTAA TCTATCAAAA GATACCTTTA TAAACCTGT      120
ATTCAAGAAA ATAGAGGAGA AAAAGGAGGA AGAAAATAAA CCTACTTTTG ATGTATCGAA      180
AAAGAAAGAT AACCCACAAG TAAACCATAG TCAATTAAAT GAAAGTCACA GAAAAGAGGA      240
TTTACAAAGA GAAGAGCATT CACAAAAATC TGATTCAACT AAGGATGTTA CAGCTACAGT      300
TCTTGATAAA AACAATATCA GTAGTAAATC AACTACTAAC AATCCTAATA AG              352

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(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 117 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Tyr Lys Gly Glu Leu Glu Lys Gly Tyr Gln Phe Asp Gly Trp Glu Ile  
 1 5 10 15

Ser Gly Phe Glu Gly Lys Lys Asp Ala Gly Tyr Val Ile Asn Leu Ser  
 20 25 30

Lys Asp Thr Phe Ile Lys Pro Val Phe Lys Lys Ile Glu Glu Lys Lys  
 35 40 45

Glu Glu Glu Asn Lys Pro Thr Phe Asp Val Ser Lys Lys Lys Asp Asn  
 50 55 60

Pro Gln Val Asn His Ser Gln Leu Asn Glu Ser His Arg Lys Glu Asp  
 65 70 75 80

Leu Gln Arg Glu Glu His Ser Gln Lys Ser Asp Ser Thr Lys Asp Val  
 85 90 95

Thr Ala Thr Val Leu Asp Lys Asn Asn Ile Ser Ser Lys Ser Thr Thr  
 100 105 110

Asn Asn Pro Asn Lys  
 115

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1312 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GAATGTTTCAG GCTCAAGAAA GTTCAGGAAA TAAAATCCAC TTTATCAATG TTCAAGAAGG 60  
 TGGCAGTGAT GCGATTATTC TTGAAAGCAA TGGACATTTT GCCATGGTGG ATACAGGAGA 120  
 AGATTATGAT TTCCCAGATG GAAGTGATTC TCGCTATCCA TGGAGAGAAG GAATTGAAAC 180  
 GTCTTATAAG CATGTTCTAA CAGACCGTGT CTTTCGTCGT TTGAAGGAAT TGGGTGTCCA 240  
 AAAACTTGAT TTTATTTTGG TGACCCATAC CCACAGTGAT CATATTGGAA ATGTTGATGA 300  
 ATTACTGTCT ACCTATCCAG TTGACCGAGT CTATCTTAAG AAATATAGTG ATAGTCGTAT 360  
 TACTAATTCT GAACGTCTAT GGGATAATCT GTATGGCTAT GATAAGGTTT TACAGACTGC 420  
 TGCAGAAAAA GGTGTTTCAG TTATTCAAAA TATCACACAA GGGGATGCTC ATTTTCAGTT 480  
 TGGGGACATG GATATTCAGC TCTATAATTA TGAAAATGAA ACTGATTCAT CGGGTGAATT 540  
 AAAGAAAATT TGGGATGACA ATTCCAATTC CTTGATTAGC GTGGTGAAAG TCAATGGCAA 600  
 GAAAATTTAC CTTGGGGGCG ATTTAGATAA TGTTTCATGGA GCAGAAGACA AGTATGGTCC 660  
 TCTCATTGGA AAAGTTGATT TGATGAAGTT TAATCATCAC CATGATACCA ACAAATCAAA 720  
 TACCAAGGAT TTCATTAAAA ATTTGAGTCC GAGTTTGATT GTTCAAACCT CGGATAGTCT 780  
 ACCTTGGA AAATGGTGTTG ATAGTGAGTA TGTTAATTGG CTCAAAGAAC GAGGAATTGA 840  
 GAGAATCAAC GCAGCCAGCA AAGACTATGA TGCAACAGTT TTTGATATTC GAAAAGACGG 900  
 TTTTGTC AAT TTTCAACAT CCTACAAGCC GATTCCAAGT TTTCAAGCTG GTTGGCATAA 960  
 GAGTGCATAT GGGAACTGGT GGTATCAAGC GCCTGATTCT ACAGGAGAGT ATGCTGTCGG 1020  
 TTGGAATGAA ATCGAAGGTG AATGGTATTA CTTTAACCAA ACGGGTATCT TGTTACAGAA 1080  
 TCAATGGAAA AAATGGAACA ATCATTTGGT CTATTTGACA GACTCTGGTG CTTCTGCTAA 1140  
 AAATTGGAAG AAAATCGCTG GAATCTGGTA TTATTTTAAC AAAGAAAACC AGATGGAAAT 1200  
 TGGTTGGATT CAAGATAAAG AGCAGTGGTA TTATTTGGAT GTTGATGGTT CTATGAAGAC 1260  
 AGGATGGCTT CAATATATGG GGCAATGGTA TTACTTTGCT CCATCAGGGG AA 1312

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asn Val Gln Ala Gln Glu Ser Ser Gly Asn Lys Ile His Phe Ile Asn

1	5	10	15
Val	Gln	Glu	Gly
	20		
Gly	Ser	Asp	Ala
			25
Ile	Ile	Leu	Glu
			30
Asn	Gly	His	
Phe	Ala	Met	Val
	35		
Asp	Thr	Gly	Glu
			40
Asp	Tyr	Asp	Phe
			45
Pro	Asp	Gly	Ser
Asp	Ser	Arg	Tyr
	50		
Pro	Trp	Arg	Glu
			55
Gly	Ile	Glu	Thr
			60
Ser	Tyr	Lys	His
Val	Leu	Thr	Asp
			70
Arg	Val	Phe	Arg
			75
Leu	Lys	Glu	Leu
Gly	Val	Gln	
			80
Lys	Leu	Asp	Phe
			85
Ile	Leu	Val	Thr
			90
His	Thr	His	Ser
Asp	His	Ile	Gly
			95
Asn	Val	Asp	Glu
			100
Leu	Leu	Ser	Thr
			105
Tyr	Pro	Val	Asp
			110
Arg	Val	Tyr	Leu
Lys	Lys	Tyr	Ser
			115
Asp	Ser	Arg	Ile
			120
Thr	Asn	Ser	Glu
			125
Arg	Leu	Trp	Asp
Asn	Leu	Tyr	Gly
			130
Tyr	Asp	Lys	Val
			135
Leu	Gln	Thr	Ala
			140
Ala	Ala	Glu	Lys
Gly	Lys	Gly	
Val	Ser	Val	Ile
			145
Gln	Asn	Ile	Thr
			150
Gly	Asp	Ala	His
			155
Phe	Gln	Phe	
			160
Gly	Asp	Met	Asp
			165
Ile	Gln	Leu	Tyr
			170
Asn	Tyr	Glu	Asn
Glu	Asn	Glu	Thr
			175
Asp	Ser		
Ser	Gly	Glu	Leu
			180
Lys	Lys	Ile	Trp
			185
Asp	Asp	Asn	Ser
			190
Asn	Ser	Asn	Ser
Ser	Val	Val	Lys
			195
Val	Asn	Gly	Lys
			200
Lys	Lys	Ile	Tyr
Leu	Gly	Gly	Asp
			205
Leu			
Asp	Asn	Val	His
			210
Gly	Ala	Glu	Asp
			215
Lys	Tyr	Gly	Pro
			220
Leu	Ile	Gly	Lys
Val	Asp	Leu	Met
			225
Lys	Phe	Asn	His
			230
His	His	His	Asp
			235
Thr	Asn	Lys	Ser
Leu	Ile	Val	Gln
			245
Thr			
Ser	Asp	Ser	Leu
			260
Pro	Trp	Lys	Asn
			265
Gly	Val	Asp	Ser
Glu	Tyr	Val	Asn
			270
Trp	Leu	Lys	Glu
			275
Arg	Gly	Ile	Glu
			280
Arg	Ile	Asn	Ala
			285
Ala	Ala	Ser	Lys
Asp	Gly	Phe	Val
			300
Tyr	Asp	Ala	Thr
			290
Val	Phe	Asp	Ile
			295
Arg	Lys	Asp	Gly
			300
Ser	Thr	Ser	Tyr
			305
Lys	Pro	Ile	Pro
			310
Ser	Phe	Gln	Ala
			315
Gly	Trp	His	Lys
			320
Ser	Ala	Tyr	Gly
			325
Asn	Trp	Trp	Tyr
Gln	Ala	Pro	Asp
			330
Ser	Thr	Gly	Glu
			335
Tyr	Ala	Val	Gly
			340
Trp	Asn	Glu	Ile
Glu	Gly	Glu	Trp
			345
Tyr	Tyr	Phe	Asn
			350

Gln Thr Gly Ile Leu Leu Gln Asn Gln Trp Lys Lys Trp Asn Asn His  
 355 360 365  
 Trp Phe Tyr Leu Thr Asp Ser Gly Ala Ser Ala Lys Asn Trp Lys Lys  
 370 375 380  
 Ile Ala Gly Ile Trp Tyr Tyr Phe Asn Lys Glu Asn Gln Met Glu Ile  
 385 390 395 400  
 Gly Trp Ile Gln Asp Lys Glu Gln Trp Tyr Tyr Leu Asp Val Asp Gly  
 405 410 415  
 Ser Met Lys Thr Gly Trp Leu Gln Tyr Met Gly Gln Trp Tyr Tyr Phe  
 420 425 430  
 Ala Pro Ser Gly Glu  
 435

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1855 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CTTGGGTGTA ACCCATATCC AGTCCTTCC AGTCTTGTCT TACTACTTTG TCAATGAATT 60  
 GAAAAACCAT GAACGCTTGT CTGACTACGC TTCAAGCAAC AGCAACTACA ACTGGGGATA 120  
 TGACCCTCAA AACTACTTCT CCTTGACTGG TATGTACTCA AGCGATCCTA AGAATCCAGA 180  
 AAAACGAATC GCAGAATTTA AAAACCTCAT CAACGAAATC CACAAACGTG GTATGGGAGC 240  
 TATCCTAGAT GTCGTTTATA ACCACACAGC CAAAGTCGAT CTCTTTGAAG ATTTGGAACC 300  
 AAATACTAC CACTTTTATGG ATGCCGATGG CACACCTCGA ACTAGCTTTG GTGGTGGACG 360  
 CTTGGGGACA ACCCACCATA TGACCAAACG GCTCCTAATT GACTCTATCA AATACCTAGT 420  
 TGATACCTAC AAAGTGGATG GCTTCCGTTT CGATATGATG GGAGACCATG ACGCCGCTTC 480  
 TATCGAAGAA GCTTACAAGG CTGCACGCGC CCTCAATCCA AACCTCATCA TGCTTGGTGA 540  
 AGGTTGGAGA ACCTATGCCG GTGATGAAAA CATGCCTACT AAAGCTGCTG ACCAAGATTG 600  
 GATGAAACAT ACCGATACTG TCGCTGTCTT TTCAGATGAC ATCCGTAACA ACCTCAAATC 660  
 TGGTTATCCA AACGAAGGTC AACCTGCCTT TATCACAGGT GGCAAGCGTG ATGTCAACAC 720  
 CATCTTTAAA AATCTCATTG CTCAACCAAC TAACTTTGAA GCTGACAGCC CTGGAGATGT 780  
 CATCCAATAC ATCGCAGCCC ATGATAACTT GACCCTCTTT GACATCATTG CCCAGTCTAT 840  
 CAAAAAGAC CCAAGCAAGG CTGAGAACTA TGCTGAAATC CACCGTCGTT TACGACTTGG 900  
 AAATCTCATG GTCTTGACAG CTCAAGGAAC TCCATTTATC CACTCCGGTC AGGAATATGG 960  
 ACGTACTAAA CAATTCCGTG ACCCAGCCTA CAAGACTCCA GTAGCAGAGG ATAAGGTTCC 1020

AAACAAATCT CACTTGTTC GTGATAAGGA CGGCAACCCA TTTGACTATC CTTACTTCAT 1080  
 CCATGACTCT TACGATTCTA GTGATGCAGT CAACAAGTTT GACTGGACTA AGGCTACAGA 1140  
 TGGTAAAGCT TATCCTGAAA ATGTCAAGAG CCGTGACTAT ATGAAAGGTT TGATTGCCCT 1200  
 TCGTCAATCT ACAGATGCCT TCCGACTTAA GAGTCTTCAA GATATCAAAG ACCGTGTCCA 1260  
 CCTCATCACT GTCCCAGGCC AAAATGGTGT GGAAAAAGAG GATGTAGTGA TTGGCTACCA 1320  
 AATCACTGCT CCAAACGGCG ATATCTACGC AGTCTTTGTC AATGCGGATG AAAAAGCTCG 1380  
 CGAATTTAAT TTGGGAAC TG CCTTTGCACA TCTAAGAAAT GCGGAAGTTT TGGCAGATGA 1440  
 AAACCAAGCA GGACCAGTCG GAATTGCCAA CCCGAAAGGA CTTGAATGGA CTGAAAAAGG 1500  
 CTTGAAATTG AATGCCCTTA CAGCTACTGT TCTTCGAGTC TCTCAAAATG GAACTAGCCA 1560  
 TGAGTCAACT GCAGAAGAGA AACCAGACTC AACCCCTTCC AAGCCTGAAC ATCAAAATGA 1620  
 AGCTTCTCAC CCTGCACATC AAGACCCAGC TCCAGAAGCT AGACCTGATT CTACTAAACC 1680  
 AGATGCCAAA GTAGCTGATG CGGAAAATAA ACCTAGCCAA GCTACAGCTG ATTACAAGC 1740  
 TGAACAACCA GCACAAGAAG CACAAGCATC ATCTGTAAAA GAAGCGGTTT GAAACGAATC 1800  
 GGTAGAAAAC TCTAGCAAGG AAAATATACC TGCAACCCCA GATAACAAG CTGAA 1855

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Gly Val Thr His Ile Gln Leu Leu Pro Val Leu Ser Tyr Tyr Phe  
 1 5 10 15  
 Val Asn Glu Leu Lys Asn His Glu Arg Leu Ser Asp Tyr Ala Ser Ser  
 20 25 30  
 Asn Ser Asn Tyr Asn Trp Gly Tyr Asp Pro Gln Asn Tyr Phe Ser Leu  
 35 40 45  
 Thr Gly Met Tyr Ser Ser Asp Pro Lys Asn Pro Glu Lys Arg Ile Ala  
 50 55 60  
 Glu Phe Lys Asn Leu Ile Asn Glu Ile His Lys Arg Gly Met Gly Ala  
 65 70 75 80  
 Ile Leu Asp Val Val Tyr Asn His Thr Ala Lys Val Asp Leu Phe Glu  
 85 90 95  
 Asp Leu Glu Pro Asn Tyr Tyr His Phe Met Asp Ala Asp Gly Thr Pro  
 100 105 110  
 Arg Thr Ser Phe Gly Gly Gly Arg Leu Gly Thr Thr His His Met Thr

115					120					125					
Lys	Arg	Leu	Leu	Ile	Asp	Ser	Ile	Lys	Tyr	Leu	Val	Asp	Thr	Tyr	Lys
	130					135					140				
Val	Asp	Gly	Phe	Arg	Phe	Asp	Met	Met	Gly	Asp	His	Asp	Ala	Ala	Ser
145					150					155					160
Ile	Glu	Glu	Ala	Tyr	Lys	Ala	Ala	Arg	Ala	Leu	Asn	Pro	Asn	Leu	Ile
				165					170					175	
Met	Leu	Gly	Glu	Gly	Trp	Arg	Thr	Tyr	Ala	Gly	Asp	Glu	Asn	Met	Pro
			180					185					190		
Thr	Lys	Ala	Ala	Asp	Gln	Asp	Trp	Met	Lys	His	Thr	Asp	Thr	Val	Ala
		195					200					205			
Val	Phe	Ser	Asp	Asp	Ile	Arg	Asn	Asn	Leu	Lys	Ser	Gly	Tyr	Pro	Asn
	210					215					220				
Glu	Gly	Gln	Pro	Ala	Phe	Ile	Thr	Gly	Gly	Lys	Arg	Asp	Val	Asn	Thr
225					230					235					240
Ile	Phe	Lys	Asn	Leu	Ile	Ala	Gln	Pro	Thr	Asn	Phe	Glu	Ala	Asp	Ser
				245					250					255	
Pro	Gly	Asp	Val	Ile	Gln	Tyr	Ile	Ala	Ala	His	Asp	Asn	Leu	Thr	Leu
			260					265					270		
Phe	Asp	Ile	Ile	Ala	Gln	Ser	Ile	Lys	Lys	Asp	Pro	Ser	Lys	Ala	Glu
		275					280					285			
Asn	Tyr	Ala	Glu	Ile	His	Arg	Arg	Leu	Arg	Leu	Gly	Asn	Leu	Met	Val
	290					295					300				
Leu	Thr	Ala	Gln	Gly	Thr	Pro	Phe	Ile	His	Ser	Gly	Gln	Glu	Tyr	Gly
305					310					315					320
Arg	Thr	Lys	Gln	Phe	Arg	Asp	Pro	Ala	Tyr	Lys	Thr	Pro	Val	Ala	Glu
				325					330					335	
Asp	Lys	Val	Pro	Asn	Lys	Ser	His	Leu	Leu	Arg	Asp	Lys	Asp	Gly	Asn
			340					345					350		
Pro	Phe	Asp	Tyr	Pro	Tyr	Phe	Ile	His	Asp	Ser	Tyr	Asp	Ser	Ser	Asp
		355					360					365			
Ala	Val	Asn	Lys	Phe	Asp	Trp	Thr	Lys	Ala	Thr	Asp	Gly	Lys	Ala	Tyr
	370					375					380				
Pro	Glu	Asn	Val	Lys	Ser	Arg	Asp	Tyr	Met	Lys	Gly	Leu	Ile	Ala	Leu
385					390					395					400
Arg	Gln	Ser	Thr	Asp	Ala	Phe	Arg	Leu	Lys	Ser	Leu	Gln	Asp	Ile	Lys
				405					410					415	
Asp	Arg	Val	His	Leu	Ile	Thr	Val	Pro	Gly	Gln	Asn	Gly	Val	Glu	Lys
			420					425					430		
Glu	Asp	Val	Val	Ile	Gly	Tyr	Gln	Ile	Thr	Ala	Pro	Asn	Gly	Asp	Ile
		435					440					445			
Tyr	Ala	Val	Phe	Val	Asn	Ala	Asp	Glu	Lys	Ala	Arg	Glu	Phe	Asn	Leu
	450					455					460				

Gly Thr Ala Phe Ala His Leu Arg Asn Ala Glu Val Leu Ala Asp Glu  
 465 470 475 480  
 Asn Gln Ala Gly Pro Val Gly Ile Ala Asn Pro Lys Gly Leu Glu Trp  
 485 490 495  
 Thr Glu Lys Gly Leu Lys Leu Asn Ala Leu Thr Ala Thr Val Leu Arg  
 500 505 510  
 Val Ser Gln Asn Gly Thr Ser His Glu Ser Thr Ala Glu Glu Lys Pro  
 515 520 525  
 Asp Ser Thr Pro Ser Lys Pro Glu His Gln Asn Glu Ala Ser His Pro  
 530 535 540  
 Ala His Gln Asp Pro Ala Pro Glu Ala Arg Pro Asp Ser Thr Lys Pro  
 545 550 555 560  
 Asp Ala Lys Val Ala Asp Ala Glu Asn Lys Pro Ser Gln Ala Thr Ala  
 565 570 575  
 Asp Ser Gln Ala Glu Gln Pro Ala Gln Glu Ala Gln Ala Ser Ser Val  
 580 585 590  
 Lys Glu Ala Val Arg Asn Glu Ser Val Glu Asn Ser Ser Lys Glu Asn  
 595 600 605  
 Ile Pro Ala Thr Pro Asp Lys Gln Ala Glu  
 610 615

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TAGTGATGGT ACTTGGCAAG GAAAACAGTA TCTGAAAGAA GATGGCAGTC AAGCAGCAAA	60
TGAGTGGGTT TTNGATACTC ATTATCAATC TTGGTTCTAT ATAAAAGCAG ATGCTAACTA	120
TGCTGAAAAT GAATGGCTAA AGCAAGGTGA CGACTATTTT TACCTCAAAT CTGGTGGCTA	180
TATGGCCAAA TCAGAAATGGG TAGAAGACAA GGGAGCCTTT TATTATCTTG ACCAAGATGG	240
AAAGATGAAA AGAAATGCTT GGGTAGGAAC TTCTTATGTT GGTGCAACAG GTGCCAAAGT	300
AATAGAAGAC TGGGTCTATG ATTCTCAATA CGATGCTTGG TTTTATATCA AAGCAGATGG	360
ACAGCACGCA GAGAAAGAAT GGCTCCAAAT TAAAGGGAAG GACTATTATT TCAAATCCGG	420
TGGTTATCTA CTGACAAGTC AGTGGATTAA TCAAGCTTAT GTGAATGCTA GTGGTGCCAA	480
AGTACAGCAA GGTGGCTTTT TTGACAAACA ATACCAATCT TGGTTTTTACA TCAAAGAAAA	540
TGGAAACTAT GCTGATAAAG AATGGATTTT CGAGAATGGT CACTATTATT ATCTAAAATC	600
CGGTGGCTAC ATGGCAGCCA ATGAATGGAT TTGGGATAAG GAATCTTGGT TTTATCTCAA	660



ATTTGATGGG AAAATGGCTG AAAAAGAATG GGTCTACGAT TCTCATAGTC AAGCTTGGTA 720  
 CTACTTCAAA TCCGGTGGTT ACATGACAGC CAATGAATGG ATTTGGGATA AGGAATCTTG 780  
 GTTTTACCTC AAATCTGATG GGAAAATAGC TGAAAAAGAA TGGGTCTACG ATTCTCATAG 840  
 TCAAGCTTGG TACTACTTCA AATCTGGTGG CTACATGGCG AAAAATGAGA CAGTAGATGG 900  
 TTATCAGCTT GGAAGCGATG GTAAATGGCT TGGAGGAAAA ACTACAAATG AAAATGCTGC 960  
 TTACTATCAA GTAGTGCCTG TTACAGCCAA TGTTTATGAT TCAGATGGTG AAAAGCTTTC 1020  
 CTATATATCG CAAGGTAGTG TCGTATGGCT AGATAAGGAT AGAAAAAGTG ATGACAAGCG 1080  
 CTTGGCTATT ACTATTTCTG GTTTGTCAGG CTATATGAAA ACAGAAGATT TACAAGCGCT 1140  
 AGATGCTAGT AAGGACTTTA TCCCTTATTA TGAGAGTGAT GGCCACCGTT TTTATCACTA 1200  
 TGTGGCTCAG AATGCTAGTA TCCCAGTAGC TTCTCATCTT TCTGATATGG AAGTAGGCAA 1260  
 GAAATATTAT TCGGCAGATG GCCTGCATTT TGATGGTTTT AAGCTTGAGA ATCCCTTCCT 1320  
 TTTCAAAGAT TTAACAGAGG CTACAACTA CAGTGTCTGAA GAATTGGATA AGGTATTTAG 1380  
 TTTGCTAAAC ATTAACAATA GCCTTTTGGG GAACAAGGGC GCTACTTTTA AGGAAGCCGA 1440  
 AGAACATTAC CATATCAATG CTCTTTATCT CCTTGCCCAT AGTGCCCTAG AAAGTAACTG 1500  
 GGAAGAAGT AAAATTGCCA AAGATAAGAA TAATTTCTTT GGCATTACAG CCTATGATAC 1560  
 GACCCCTTAC CTTTCTGCTA AGACATTTGA TGATGTGGAT AAGGGAATTT TAGGTGCAAC 1620  
 CAAGTGGATT AAGGAAAATT ATATCGATAG GGGAAGAACT TTCCTTGGA ACAAGGCTTC 1680  
 TGGTATGAAT GTGGAATATG CTTTCAGACCC TTATTGGGGC GAAAAAATTG CTAGTGTGAT 1740  
 GATGAAAATC AATGAGAAGC TAGGTGGCAA AGAT 1774

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Asp Gly Thr Trp Gln Gly Lys Gln Tyr Leu Lys Glu Asp Gly Ser  
 1 5 10 15  
 Gln Ala Ala Asn Glu Trp Val Xaa Asp Thr His Tyr Gln Ser Trp Phe  
 20 25 30  
 Tyr Ile Lys Ala Asp Ala Asn Tyr Ala Glu Asn Glu Trp Leu Lys Gln  
 35 40 45  
 Gly Asp Asp Tyr Phe Tyr Leu Lys Ser Gly Gly Tyr Met Ala Lys Ser  
 50 55 60

Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp Gln Asp Gly  
 65 70 75 80  
 Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val Gly Ala Thr  
 85 90 95  
 Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln Tyr Asp Ala  
 100 105 110  
 Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys Glu Trp Leu  
 115 120 125  
 Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly Tyr Leu Leu  
 130 135 140  
 Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser Gly Ala Lys  
 145 150 155 160  
 Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser Trp Phe Tyr  
 165 170 175  
 Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile Phe Glu Asn  
 180 185 190  
 Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala Ala Asn Glu  
 195 200 205  
 Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe Asp Gly Lys  
 210 215 220  
 Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr  
 225 230 235 240  
 Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp  
 245 250 255  
 Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys  
 260 265 270  
 Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser  
 275 280 285  
 Gly Gly Tyr Met Ala Lys Asn Glu Thr Val Asp Gly Tyr Gln Leu Gly  
 290 295 300  
 Ser Asp Gly Lys Trp Leu Gly Gly Lys Thr Thr Asn Glu Asn Ala Ala  
 305 310 315 320  
 Tyr Tyr Gln Val Val Pro Val Thr Ala Asn Val Tyr Asp Ser Asp Gly  
 325 330 335  
 Glu Lys Leu Ser Tyr Ile Ser Gln Gly Ser Val Val Trp Leu Asp Lys  
 340 345 350  
 Asp Arg Lys Ser Asp Asp Lys Arg Leu Ala Ile Thr Ile Ser Gly Leu  
 355 360 365  
 Ser Gly Tyr Met Lys Thr Glu Asp Leu Gln Ala Leu Asp Ala Ser Lys  
 370 375 380  
 Asp Phe Ile Pro Tyr Tyr Glu Ser Asp Gly His Arg Phe Tyr His Tyr  
 385 390 395 400  
 Val Ala Gln Asn Ala Ser Ile Pro Val Ala Ser His Leu Ser Asp Met

405										410					415						
Glu	Val	Gly	Lys	Lys	Tyr	Tyr	Ser	Ala	Asp	Gly	Leu	His	Phe	Asp	Gly						
			420					425					430								
Phe	Lys	Leu	Glu	Asn	Pro	Phe	Leu	Phe	Lys	Asp	Leu	Thr	Glu	Ala	Thr						
		435					440					445									
Asn	Tyr	Ser	Ala	Glu	Glu	Leu	Asp	Lys	Val	Phe	Ser	Leu	Leu	Asn	Ile						
	450					455					460										
Asn	Asn	Ser	Leu	Leu	Glu	Asn	Lys	Gly	Ala	Thr	Phe	Lys	Glu	Ala	Glu						
465					470					475					480						
Glu	His	Tyr	His	Ile	Asn	Ala	Leu	Tyr	Leu	Leu	Ala	His	Ser	Ala	Leu						
				485					490					495							
Glu	Ser	Asn	Trp	Gly	Arg	Ser	Lys	Ile	Ala	Lys	Asp	Lys	Asn	Asn	Phe						
			500					505					510								
Phe	Gly	Ile	Thr	Ala	Tyr	Asp	Thr	Thr	Pro	Tyr	Leu	Ser	Ala	Lys	Thr						
		515					520					525									
Phe	Asp	Asp	Val	Asp	Lys	Gly	Ile	Leu	Gly	Ala	Thr	Lys	Trp	Ile	Lys						
	530					535					540										
Glu	Asn	Tyr	Ile	Asp	Arg	Gly	Arg	Thr	Phe	Leu	Gly	Asn	Lys	Ala	Ser						
545					550					555					560						
Gly	Met	Asn	Val	Glu	Tyr	Ala	Ser	Asp	Pro	Tyr	Trp	Gly	Glu	Lys	Ile						
				565					570					575							
Ala	Ser	Val	Met	Met	Lys	Ile	Asn	Glu	Lys	Leu	Gly	Gly	Lys	Asp							
			580					585					590								

## (2) INFORMATION FOR SEQ ID NO: 75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

TGGGATTCAA TATGTCAGAG ATGATACTAG AGATAAAGAA GAGGGAATAG AGTATGATGA	60
CGCTGACAAT GGGGATATTA TTGTAAAAGT AGCGACTAAA CCTAAGGTAG TAACCAAGAA	120
AATTTCAAGT ACGCGAATTC GTTATGAAAA AGATGAAACA AAAGACCGTA GTGAAAATCC	180
TGTTACAATT GATGGAGAGG ATGGCTATGT AACTACGACA AGGACCTACG ATGTTAATCC	240
AGAGACTGGT TATGTTACCG AACAGGTTAC TGTTGATAGA AAAGAAGCCA CGGATACAGT	300
TATCAAAGTT CCAGCTAAAA GCAAGGTTGA AGAAGTTCCTT GTTCCATTTG CTACTAAATA	360
TGAAGCAGAC AATGACCTTT CTGCAGGACA GGAGCAAGAG ATTACTCTAG GAAAGAATGG	420
GAAAACAGTT ACAACGATAA CTTATAATGT AGATGGAAAG AGTGGACAAG TAACTGAGAG	480
TACTTTAAGT CAAAAAAG ACTCTCAAAC AAGAGTTGTT AAAAAAGaA CCArkCCCCA	540

AGTTCCTTGTC CAAGAAATTC CAATCGAAAC AGAATATCTC GATGGCCCaA CTCTTGATAA 600  
AaGTCAAGAA GTAGAAGAAG TAGGAGAAAT TGGTAAATTA CTCTTACTAC AATCTATACT 660  
GGTAGATGAA CGTGATGGAA CAATTGAAGA AACTACTTCT CGTCAAATTA CTAAAGAGAT 720  
GGTAAAAAGA CGTATAAGGA GAGGGACGAG AGAACCTGAA AAAGTTGTTG TTCCTGAGCA 780  
ATCATCTATT CCTTCGTATC CTGTATCTGT TACATCTAAC CAAGGAACAG ATGTAGCAGT 840  
AGAACCAGCT AAAGCAGTTG CTCCAACAAC AGACTGGAAA CAAGAAAATG GTATGTGGTA 900  
TTTTTATAAT ACTGATGGTT CCATGGCAAC AGGTTGGGTA CAAGTTAATA GTTCATGGTA 960  
CTACCTCAAC AGCAACGGTT CTATGAAAGT CAATCAATGG TTCCAAGTTG GTGGTAAATG 1020  
GTATTATGTA AATACATCGG GTGAGTTAGC GGTCAATACA AGTATAGATG GCTATAGAGT 1080  
CAATGATAAT GGTGAATGGG TGCCT 1105

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Gly Ile Gln Tyr Val Arg Asp Asp Thr Arg Asp Lys Glu Glu Gly Ile  
1 5 10 15  
Glu Tyr Asp Asp Ala Asp Asn Gly Asp Ile Ile Val Lys Val Ala Thr  
20 25 30  
Lys Pro Lys Val Val Thr Lys Lys Ile Ser Ser Thr Arg Ile Arg Tyr  
35 40 45  
Glu Lys Asp Glu Thr Lys Asp Arg Ser Glu Asn Pro Val Thr Ile Asp  
50 55 60  
Gly Glu Asp Gly Tyr Val Thr Thr Thr Arg Thr Tyr Asp Val Asn Pro  
65 70 75 80  
Glu Thr Gly Tyr Val Thr Glu Gln Val Thr Val Asp Arg Lys Glu Ala  
85 90 95  
Thr Asp Thr Val Ile Lys Val Pro Ala Lys Ser Lys Val Glu Glu Val  
100 105 110  
Leu Val Pro Phe Ala Thr Lys Tyr Glu Ala Asp Asn Asp Leu Ser Ala  
115 120 125  
Gly Gln Glu Gln Glu Ile Thr Leu Gly Lys Asn Gly Lys Thr Val Thr  
130 135 140  
Thr Ile Thr Tyr Asn Val Asp Gly Lys Ser Gly Gln Val Thr Glu Ser  
145 150 155 160

Thr Leu Ser Gln Lys Lys Asp Ser Gln Thr Arg Val Val Lys Lys Arg  
 165 170 175  
 Thr Xaa Pro Gln Val Leu Val Gln Glu Ile Pro Ile Glu Thr Glu Tyr  
 180 185 190  
 Leu Asp Gly Pro Thr Leu Asp Lys Ser Gln Glu Val Glu Glu Val Gly  
 195 200 205  
 Glu Ile Gly Lys Leu Leu Leu Gln Ser Ile Leu Val Asp Glu Arg  
 210 215 220  
 Asp Gly Thr Ile Glu Glu Thr Thr Ser Arg Gln Ile Thr Lys Glu Met  
 225 230 235 240  
 Val Lys Arg Arg Ile Arg Arg Gly Thr Arg Glu Pro Glu Lys Val Val  
 245 250 255  
 Val Pro Glu Gln Ser Ser Ile Pro Ser Tyr Pro Val Ser Val Thr Ser  
 260 265 270  
 Asn Gln Gly Thr Asp Val Ala Val Glu Pro Ala Lys Ala Val Ala Pro  
 275 280 285  
 Thr Thr Asp Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr  
 290 295 300  
 Asp Gly Ser Met Ala Thr Gly Trp Val Gln Val Asn Ser Ser Trp Tyr  
 305 310 315 320  
 Tyr Leu Asn Ser Asn Gly Ser Met Lys Val Asn Gln Trp Phe Gln Val  
 325 330 335  
 Gly Gly Lys Trp Tyr Tyr Val Asn Thr Ser Gly Glu Leu Ala Val Asn  
 340 345 350  
 Thr Ser Ile Asp Gly Tyr Arg Val Asn Asp Asn Gly Glu Trp Val Arg  
 355 360 365

## (2) INFORMATION FOR SEQ ID NO: 77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GGATAATAGA GAAGCATTA AAACCTTTAT GACGGGTGAA AATTTTATC TCCAACATTA	60
TCTAGGAGCA CATAGGGAAG AACTAAATGG AGAGCATGGC TATACCTTCC GTGTTTGGGC	120
ACCTAATGCT CAGGCTGTTT ACTTGGTTGG TGATTTTACC AACTGGATTG AAAATCAGAT	180
TCCAATGGTA AGAAATGATT TTGGGGTCTG GGAAGTCTTT ACCAATATGG CTCAAGAAGG	240
GCATATTTAC AAATATCATG TCACACGTCA AAATGGTCAT CAACTGATGA AGATTGACCC	300
TTTTGCTGTC AGGTATGAGG CTCGTCCAGG AACAGGGGCA ATCGTAACAG AGCTTCCTGA	360
GAAGAAATGG AAGGATGGAC TTTGGCTGGC ACGAAGAAAA CGTTGGGGCT TTGAAGAGCG	420

TCCTGTCAAT ATTTATGAAG TTCACGCTGG ATCATGGAAA AGAAATTCTG ATGGCAGTCC 480  
 TTATAGTTTT GCCCAGCTCA AGGATGAACT CATTCCTTAT CTCGTTGAAA TGAACATAC 540  
 TCATATTGAG TTTATGCCCT TGATGTCCCA TCCTTTGGGC TTGAGTTGGG GGTATCAGCT 600  
 TATGGGTTAC TTCGCTTTAG AGCATGCTTA TGGCCGACCA GAGGAGTTTC AAGATTTTGT 660  
 C 661

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asp Asn Arg Glu Ala Leu Lys Thr Phe Met Thr Gly Glu Asn Phe Tyr  
 1 5 10 15  
 Leu Gln His Tyr Leu Gly Ala His Arg Glu Glu Leu Asn Gly Glu His  
 20 25 30  
 Gly Tyr Thr Phe Arg Val Trp Ala Pro Asn Ala Gln Ala Val His Leu  
 35 40 45  
 Val Gly Asp Phe Thr Asn Trp Ile Glu Asn Gln Ile Pro Met Val Arg  
 50 55 60  
 Asn Asp Phe Gly Val Trp Glu Val Phe Thr Asn Met Ala Gln Glu Gly  
 65 70 75 80  
 His Ile Tyr Lys Tyr His Val Thr Arg Gln Asn Gly His Gln Leu Met  
 85 90 95  
 Lys Ile Asp Pro Phe Ala Val Arg Tyr Glu Ala Arg Pro Gly Thr Gly  
 100 105 110  
 Ala Ile Val Thr Glu Leu Pro Glu Lys Lys Trp Lys Asp Gly Leu Trp  
 115 120 125  
 Leu Ala Arg Arg Lys Arg Trp Gly Phe Glu Glu Arg Pro Val Asn Ile  
 130 135 140  
 Tyr Glu Val His Ala Gly Ser Trp Lys Arg Asn Ser Asp Gly Ser Pro  
 145 150 155 160  
 Tyr Ser Phe Ala Gln Leu Lys Asp Glu Leu Ile Pro Tyr Leu Val Glu  
 165 170 175  
 Met Asn Tyr Thr His Ile Glu Phe Met Pro Leu Met Ser His Pro Leu  
 180 185 190  
 Gly Leu Ser Trp Gly Tyr Gln Leu Met Gly Tyr Phe Ala Leu Glu His  
 195 200 205  
 Ala Tyr Gly Arg Pro Glu Glu Phe Gln Asp Phe Val

210

215


220

## (2) INFORMATION FOR SEQ ID NO: 79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:



```

AGATTTTGTGTC GAGGAGTGTGTC ATACCCATAA TATTGGGGTT ATTGTGGACT GGGTACCAGN      60
TCACTTTTACC ATCAACGATG ATGCCTTAGC CTATTATGAT GGGACACCGA CTTTGAATA      120
CCAAGACCAT AATAAGGCTC ATAACCATGG TTGGGGTGCC CTTAATTTTG ACCTTGGAAA      180
AAATGAAGTC CAGTCCTTCT TAATTTCTTG CATTAAGCAT TGGATTGATG TCTATCATTT      240
GGATGGTATT CGTGTGGATG CTGTTAGCAA CATGCTCTAT TTGGACTATG ATGATGCTCC      300
ATGGACACCT AATAAAGATG GCGGAAATCT CAACTATGAA GGTATTATT TCCTTCAGCG      360
CTTGAATGAG GTTATTAAGT TAGAATATCC AGATGTGATG ATGATTGCAG AAGAAAGTTC      420
GTCTGCGATC AAGATTACGG GAATGAAAGA GATTGGTGGT CTAGGATTTG ACTACAAATG      480
GAACATGGGC TGGATGAATG ATATCCTCCG TTTCTACGAA GAAGATCCGA TCTATCGTAA      540
ATATGACTTT AACCTGGTGA CTTTCAGCTT TATGTATGTT TNCAAGGAGA ATTATCTCTT      600
GCCATTCTCG CACGATGAAG TGGTTCATGG CAAGAAGAGT ATGATGCATA AGATGTGGGG      660
AGATCGTTAC AATCAATTTC CAGGCTTGCG CAATCTCTAT ACGTACCAA TTTGTACACC      720
TGGTAAGAAA TTGCTCTTCA TGGGTAGCGA ATACGGTCAA TTCCTAGAAT GGAAATCTGA      780
AGAACAGTTG GAATGGTCTA ACCTAGAAGA CCCAATGAAT GCTAAGATGA AGTATTTTCGC      840
TTCTCAGCTA AACCAGTTTT ACAAAGATCA TCGCTGTCTG TGGGAAATTG ATACCAGCTA      900
TGATGGTATT GAAATCATTG ATGCGGATAA TCGAGACCAG AGTGTTCCTT CCTTTATTCG      960
TAAGGGTAAA AAGGGA                                         976

```

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

Asp Phe Val Glu Glu Cys His Thr His Asn Ile Gly Val Ile Val Asp
1           5           10           15

```

Trp Val Pro Xaa His Phe Thr Ile Asn Asp Asp Ala Leu Ala Tyr Tyr  
 20 25 30  
 Asp Gly Thr Pro Thr Phe Glu Tyr Gln Asp His Asn Lys Ala His Asn  
 35 40 45  
 His Gly Trp Gly Ala Leu Asn Phe Asp Leu Gly Lys Asn Glu Val Gln  
 50 55 60  
 Ser Phe Leu Ile Ser Cys Ile Lys His Trp Ile Asp Val Tyr His Leu  
 65 70 75 80  
 Asp Gly Ile Arg Val Asp Ala Val Ser Asn Met Leu Tyr Leu Asp Tyr  
 85 90 95  
 Asp Asp Ala Pro Trp Thr Pro Asn Lys Asp Gly Gly Asn Leu Asn Tyr  
 100 105 110  
 Glu Gly Tyr Tyr Phe Leu Gln Arg Leu Asn Glu Val Ile Lys Leu Glu  
 115 120 125  
 Tyr Pro Asp Val Met Met Ile Ala Glu Glu Ser Ser Ser Ala Ile Lys  
 130 135 140  
 Ile Thr Gly Met Lys Glu Ile Gly Gly Leu Gly Phe Asp Tyr Lys Trp  
 145 150 155 160  
 Asn Met Gly Trp Met Asn Asp Ile Leu Arg Phe Tyr Glu Glu Asp Pro  
 165 170 175  
 Ile Tyr Arg Lys Tyr Asp Phe Asn Leu Val Thr Phe Ser Phe Met Tyr  
 180 185 190  
 Val Xaa Lys Glu Asn Tyr Leu Leu Pro Phe Ser His Asp Glu Val Val  
 195 200 205  
 His Gly Lys Lys Ser Met Met His Lys Met Trp Gly Asp Arg Tyr Asn  
 210 215 220  
 Gln Phe Ala Gly Leu Arg Asn Leu Tyr Thr Tyr Gln Ile Cys His Pro  
 225 230 235 240  
 Gly Lys Lys Leu Leu Phe Met Gly Ser Glu Tyr Gly Gln Phe Leu Glu  
 245 250 255  
 Trp Lys Ser Glu Glu Gln Leu Glu Trp Ser Asn Leu Glu Asp Pro Met  
 260 265 270  
 Asn Ala Lys Met Lys Tyr Phe Ala Ser Gln Leu Asn Gln Phe Tyr Lys  
 275 280 285  
 Asp His Arg Cys Leu Trp Glu Ile Asp Thr Ser Tyr Asp Gly Ile Glu  
 290 295 300  
 Ile Ile Asp Ala Asp Asn Arg Asp Gln Ser Val Leu Ser Phe Ile Arg  
 305 310 315 320  
 Lys Gly Lys Lys Gly  
 325

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2134 base pairs



(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ATCTGTAGTT TATGCGGATG AAACACTTAT TACTCATACT GCTGAGAAAC CTAAAGAGGA 60  
 AAAAATGATA GTAGAAGAAA AGGCTGATAA AGCTTTGGAA ACTAAAAATA TAGTTGAAAG 120  
 GACAGAACAA AGTGAACCTA GTTCAACTGA GGCTATTGCA TCTGAGNAGA AAGAAGATGA 180  
 AGCCGTAAC T CCAAAAGAGG AAAAAGTGTC TGCTAAACCG GAAGAAAAAG CTCCAAGGAT 240  
 AGAATCACAA GCTTCAAATC AAGAAAAACC GCTCAAGGAA GATGCTAAAG CTGTAACAAA 300  
 TGAAGAAGTG AATCAAATGA TTGAAGACAG GAAAGTGGAT TTTAATCAAA ATTGGTACTT 360  
 TAAACTCAAT GCAAATTC TA AGGAAGCCAT TAAACCTGAT GCAGACGTAT CTACGTGGAA 420  
 AAAATTAGAT TTACCGTATG ACTGGAGTAT CTTTAACGAT TTCGATCATG AATCTCCTGC 480  
 ACAAATGAA GGTGGACAGC TCAACGGTGG GGAAGCTTGG TATCGCAAGA CTTTCAAAC T 540  
 AGATGAAAAA GACCTCAAGA AAAATGTTCG CCTTACTTTT GATGGCGTCT ACATGGATTC 600  
 TCAAGTTTAT GTCAATGGTC AGTTAGTGGG GCATTATCCA AATGGTTATA ACCAGTTCTC 660  
 ATATGATATC ACCAAATACC TTCAAAAAGA TGGTCGTGAG AATGTGATTG CTGTCCATGC 720  
 AGTCAACAAA CAGCCAAGTA GCCGTTGGTA TTCAGGAAGT GGTATCTATC GTGATGTGAC 780  
 TTTACAAGTG ACAGATAAGG TGCATGTTGA GAAAAATGGG ACAACTATTT TAACACCAAA 840  
 ACTTGAAGAA CAACAACATG GCAAGGTTGA AACTCATGTG ACCAGCAAAA TCGTCAATAC 900  
 GGACGACAAA GACCATGAAC TTGTAGCCGA ATATCAAATC GTTGAACGAG GTGGTCATGC 960  
 TGTAACAGGC TTAGTTCGTA CAGCGAGTCG TACCTTAAAA GCACATGAAT CAACAAGCCT 1020  
 AGATGCGATT TTAGAAGTTG AAAGACCAAA ACTCTGGACT GTTTTAAATG ACAAACCTGC 1080  
 CTTGTACGAA TTGATTACGC GTGTTTACCG TGACGGTCAA TTGGTTGATG CTAAGAAGGA 1140  
 TTTGTTTGGT TACCGTTACT ATCACTGGAC TCCAAATGAA GGTTCCTCTT TGAATGGTGA 1200  
 ACGTATTAAA TTCCATGGAG TATCCTTGCA CCACGACCAT GGGGCGCTTG GAGCAGAAGA 1260  
 AAACTATAAA GCAGAATATC GCCGTCTCAA ACAAATGAAG GAGATGGGAG TTAACCTCAT 1320  
 CCGTACAACC CACAACCCCTG CTAGTGAGCA AACCTTGCAA ATCGCAGCAG AACTAGGTTT 1380  
 ACTCGTTCAG GAAGAGGCCT TTGATACGTG GTATGGTGGC AAGAAACCTT ATGACTATGG 1440  
 ACGTTTCTTT GAAAAAGATG CCACTCACCC AGAAGCTCGA AAAGGTGAAA AATGGTCTGA 1500  
 TTTTGACCTA CGTACCATGG TCGAAAGAGG CAAAAACAAC CCTGCTATCT TCATGTGGTC 1560  
 AATTGGTAAT GAAATAGGTG AAGCTAATGG TGATGCCAC TCTTTAGCAA CTGTAAACG 1620  
 TTTGGTTAAG GTTATCAAGG ATGTTGATAA GACTCGCTAT GTTACCATGG GAGCAGATAA 1680

ATTCCGTTTC GGTAATGGTA GCGGAGGGCA TGAGAAAATT GCTGATGAAC TCGATGCTGT 1740  
 TGGATTTAAC TATTCTGAAG ATAATTACAA AGCCCTTAGA GCTAAGCATC CAAAATGGTT 1800  
 GATTTATGGA TCAGAAACAT CTTTACGCTAC CCGTACACGT GGAAGTTACT ATCGCCCTGA 1860  
 ACGTGAATTG AAACATAGCA ATGGACCTGA GCGTAATTAT GAACAGTCAG ATTATGGAAA 1920  
 TGATCGTGTG GGTGGGGGA AAACAGCAAC CGCTTCATGG ACTTTTGACC GTGACAACGC 1980  
 TGGCTATGCT GGACAGTTTA TCTGGACAGG TACGGACTAT ATTGGTGAAC CTACACCATG 2040  
 GCACAACCAA AATCAAACCTC CTGTTAAGAG CTCTTACTTT GGTATCGTAG ATACAGCCGG 2100  
 CATTCCAAAA CATGACTTCT ATCTCTACCA AAGC 2134

(2) INFORMATION FOR SEQ ID NO:82:


- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 711 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser Val Val Tyr Ala Asp Glu Thr Leu Ile Thr His Thr Ala Glu Lys  
 1 5 10 15  
 Pro Lys Glu Glu Lys Met Ile Val Glu Glu Lys Ala Asp Lys Ala Leu  
 20 25 30  
 Glu Thr Lys Asn Ile Val Glu Arg Thr Glu Gln Ser Glu Pro Ser Ser  
 35 40 45  
 Thr Glu Ala Ile Ala Ser Glu Xaa Lys Glu Asp Glu Ala Val Thr Pro  
 50 55 60  
 Lys Glu Glu Lys Val Ser Ala Lys Pro Glu Glu Lys Ala Pro Arg Ile  
 65 70 75 80  
 Glu Ser Gln Ala Ser Asn Gln Glu Lys Pro Leu Lys Glu Asp Ala Lys  
 85 90 95  
 Ala Val Thr Asn Glu Glu Val Asn Gln Met Ile Glu Asp Arg Lys Val  
 100 105 110  
 Asp Phe Asn Gln Asn Trp Tyr Phe Lys Leu Asn Ala Asn Ser Lys Glu  
 115 120 125  
 Ala Ile Lys Pro Asp Ala Asp Val Ser Thr Trp Lys Lys Leu Asp Leu  
 130 135 140  
 Pro Tyr Asp Trp Ser Ile Phe Asn Asp Phe Asp His Glu Ser Pro Ala  
 145 150 155 160  
 Gln Asn Glu Gly Gly Gln Leu Asn Gly Gly Glu Ala Trp Tyr Arg Lys  
 165 170 175  
 Thr Phe Lys Leu Asp Glu Lys Asp Leu Lys Lys Asn Val Arg Leu Thr  
 180 185 190

Phe Asp Gly Val Tyr Met Asp Ser Gln Val Tyr Val Asn Gly Gln Leu  
 195 200 205  
 Val Gly His Tyr Pro Asn Gly Tyr Asn Gln Phe Ser Tyr Asp Ile Thr  
 210 215 220  
 Lys Tyr Leu Gln Lys Asp Gly Arg Glu Asn Val Ile Ala Val His Ala  
 225 230 235 240  
 Val Asn Lys Gln Pro Ser Ser Arg Trp Tyr Ser Gly Ser Gly Ile Tyr  
 245 250 255  
 Arg Asp Val Thr Leu Gln Val Thr Asp Lys Val His Val Glu Lys Asn  
 260 265 270  
 Gly Thr Thr Ile Leu Thr Pro Lys Leu Glu Glu Gln Gln His Gly Lys  
 275 280 285  
 Val Glu Thr His Val Thr Ser Lys Ile Val Asn Thr Asp Asp Lys Asp  
 290 295 300  
 His Glu Leu Val Ala Glu Tyr Gln Ile Val Glu Arg Gly Gly His Ala  
 305 310 315 320  
 Val Thr Gly Leu Val Arg Thr Ala Ser Arg Thr Leu Lys Ala His Glu  
 325 330 335  
 Ser Thr Ser Leu Asp Ala Ile Leu Glu Val Glu Arg Pro Lys Leu Trp  
 340 345 350  
 Thr Val Leu Asn Asp Lys Pro Ala Leu Tyr Glu Leu Ile Thr Arg Val  
 355 360 365  
 Tyr Arg Asp Gly Gln Leu Val Asp Ala Lys Lys Asp Leu Phe Gly Tyr  
 370 375 380  
 Arg Tyr Tyr His Trp Thr Pro Asn Glu Gly Phe Ser Leu Asn Gly Glu  
 385 390 395 400  
 Arg Ile Lys Phe His Gly Val Ser Leu His His Asp His Gly Ala Leu  
 405 410 415  
 Gly Ala Glu Glu Asn Tyr Lys Ala Glu Tyr Arg Arg Leu Lys Gln Met  
 420 425 430  
 Lys Glu Met Gly Val Asn Ser Ile Arg Thr Thr His Asn Pro Ala Ser  
 435 440 445  
 Glu Gln Thr Leu Gln Ile Ala Ala Glu Leu Gly Leu Leu Val Gln Glu  
 450 455 460  
 Glu Ala Phe Asp Thr Trp Tyr Gly Gly Lys Lys Pro Tyr Asp Tyr Gly  
 465 470 475 480  
 Arg Phe Phe Glu Lys Asp Ala Thr His Pro Glu Ala Arg Lys Gly Glu  
 485 490 495  
 Lys Trp Ser Asp Phe Asp Leu Arg Thr Met Val Glu Arg Gly Lys Asn  
 500 505 510  
 Asn Pro Ala Ile Phe Met Trp Ser Ile Gly Asn Glu Ile Gly Glu Ala  
 515 520 525




Asn Gly Asp Ala His Ser Leu Ala Thr Val Lys Arg Leu Val Lys Val  
 530 535 540  
 Ile Lys Asp Val Asp Lys Thr Arg Tyr Val Thr Met Gly Ala Asp Lys  
 545 550 555 560  
 Phe Arg Phe Gly Asn Gly Ser Gly Gly His Glu Lys Ile Ala Asp Glu  
 565 570 575  
 Leu Asp Ala Val Gly Phe Asn Tyr Ser Glu Asp Asn Tyr Lys Ala Leu  
 580 585 590  
 Arg Ala Lys His Pro Lys Trp Leu Ile Tyr Gly Ser Glu Thr Ser Ser  
 595 600 605  
 Ala Thr Arg Thr Arg Gly Ser Tyr Tyr Arg Pro Glu Arg Glu Leu Lys  
 610 615 620  
 His Ser Asn Gly Pro Glu Arg Asn Tyr Glu Gln Ser Asp Tyr Gly Asn  
 625 630 635 640  
 Asp Arg Val Gly Trp Gly Lys Thr Ala Thr Ala Ser Trp Thr Phe Asp  
 645 650 655  
 Arg Asp Asn Ala Gly Tyr Ala Gly Gln Phe Ile Trp Thr Gly Thr Asp  
 660 665 670  
 Tyr Ile Gly Glu Pro Thr Pro Trp His Asn Gln Asn Gln Thr Pro Val  
 675 680 685  
 Lys Ser Ser Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His  
 690 695 700  
 Asp Phe Tyr Leu Tyr Gln Ser  
 705 710

## (2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2167 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTACTTTGGT ATCGTAGATA CAGCCGGCAT TCCAAAACAT GACTTCTATC TCTACCAAAG	60
CCAATGGGTT TCTGTTAAGA AGAAACCGAT GGTACACCTT CTTCCCTCACT GGAAGTGGGA	120
AAACAAAGAA TTAGCATCCA AAGTAGCTGA CTCAGAAGGT AAGATTCCAG TTCGTGCTTA	180
TTCGAATGCT TCTAGTGTAG AATTGTTCTT GAATGGAAAA TCTCTTGGTC TTAAGACTTT	240
CAATAAAAAA CAAACCAGCG ATGGGCGGAC TTACCAAGAA GGTGCAAATG CTAATGAACT	300
TTATCTTGAA TGGAAGTTG CCTATCAACC AGGTACCTTG GAAGCAATTG CTCGTGATGA	360
ATCTGGCAAG GAAATTGCTC GAGATAAGAT TACGACTGCT GGTAAGCCAG CGGCAGTTCG	420
TCTTATTAAG GAAGACCATG CGATTGCAGC AGATGGAAAA GACTTGACTT ACATCTACTA	480



TGAAATTGTT GACAGCCAGG GGAATGTGGT TCCAAC TGCT AATAATCTGG TTCGCTTCCA	540
ATTGCATGGC CAAGGTCAAC TGGTCGGTGT AGATAACGGA GAACAAGCCA GCCGTGAACG	600
CTATAAGGCG CAAGCAGATG GTTCTTGGAT TCGTAAAGCA TTTAATGGTA AAGGTGTTGC	660
CATTGTCAAA TCAACTGAAC AAGCAGGAA ATTCAACCTG ACTGCCCCACT CTGATCTCTT	720
GAAATCGAAC CAAGTCACTG TCTTTACTGG TAAGAAAGAA GGACAAGAGA AGACTGTTTT	780
GGGGACAGAA GTGCCAAAAG TACAGACCAT TATTGGAGAG GCACCTGAAA TGCCTACCAC	840
TGTTCCGTTT GTATACAGTG ATGGTAGCCG TGCAGAACGT CCTGTAACCT GGTCTTCAGT	900
AGATGTGAGC AAGCCTGGTA TTGTAACGGT GAAAGGTATG GCTGACGGAC GAGAAGTAGA	960
AGCTCGTGTA GAAGTGATTG CTCTTAAATC AGAGCTACCA GTTGTGAAAC GTATTGCTCC	1020
AAATACTGAC TTGAATTCTG TAGACAAATC TGTTTCCTAT GTTTTGATTG ATGGAAGTGT	1080
TGAAGAGTAT GAAGTGGACA AGTGGGAGAT TGCCGAAGAA GATAAAGCTA AGTTAGCAAT	1140
TCCAGGTTCT CGTATTCAAG CGACCGGTTA TTTAGAAGGT CAACCAATTC ATGCAACCCT	1200
TGTGGTAGAA GAAGGCAATC CTGCGGCACC TGCAGTACCA ACTGTAACGG TTGGTGGTGA	1260
GGCAGTAACA GGTCTTACTA GTCAAAAACC AATGCAATAC CGCACTCTTG CTTATGGAGC	1320
TAAGTTGCCA GAAGTCACAG CAAGTGCTAA AAATGCAGCT GTTACAGTTC TTCAAGCAAG	1380
CGCAGCAAAC GGCATGCGTG CGAGCATCTT TATTCAGCCT AAAGATGGTG GCCCTCTTCA	1440
AACCTATGCA ATTCAATTCC TTGAAGAAGC GCCAAAAATT GCTCACTTGA GCTTGCAAGT	1500
GGAAAAAGCT GACAGTCTCA AAGAAGACCA AACTGTCAAA TTGTCGGTTC GAGCTCACTA	1560
TCAAGATGGA ACGCAAGCTG TATTACCAGC TGATAAAGTA ACCTTCTCTA CAAGTGGTGA	1620
AGGGGAAGTC GCAATTCTGT AAGGAATGCT TGAGTTGCAT AAGCCAGGAG CAGTCACTCT	1680
GAACGCTGAA TATGAGGGAG CTAAAGACCA AGTTGAACTC ACTATCCAAG CCAATACTGA	1740
GAAGAAGATT GCGCAATCCA TCCGTCTGT AAATGTAGTG ACAGATTTGC ATCAGGAACC	1800
AAGTCTTCCA GCAACAGTAA CAGTTGAGTA TGACAAAGGT TTCCCTAAAA CTCATAAAGT	1860
CACTTGGCAA GCTATTCCGA AAGAAAACT AGACTCCTAT CAAACATTTG AAGTACTAGG	1920
TAAAGTTGAA GGAATTGACC TTGAAGCGCG TGCAAAAGTC TCTGTAGAAG GTATCGTTTC	1980
AGTTGAAGAA GTCAGTGTTA CAACTCCAAT CGCAGAAGCA CCACAATTAC CAGAAAGTGT	2040
TCGGACATAT GATTCAAATG GTCACGTTTC ATCAGCTAAG GTTGCATGGG ATGCGATTTCG	2100
TCCAGAGCAA TACGCTAAGG AAGGTGTCTT TACAGTTAAT GGTGCTTAG AAGGTACGCA	2160
ATTAACA	2167

## (2) INFORMATION FOR SEQ ID NO:84:


## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:



Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His Asp Phe Tyr  
 1 5 10 15  
 Leu Tyr Gln Ser Gln Trp Val Ser Val Lys Lys Lys Pro Met Val His  
 20 25 30  
 Leu Leu Pro His Trp Asn Trp Glu Asn Lys Glu Leu Ala Ser Lys Val  
 35 40 45  
 Ala Asp Ser Glu Gly Lys Ile Pro Val Arg Ala Tyr Ser Asn Ala Ser  
 50 55 60  
 Ser Val Glu Leu Phe Leu Asn Gly Lys Ser Leu Gly Leu Lys Thr Phe  
 65 70 75 80  
 Asn Lys Lys Gln Thr Ser Asp Gly Arg Thr Tyr Gln Glu Gly Ala Asn  
 85 90 95  
 Ala Asn Glu Leu Tyr Leu Glu Trp Lys Val Ala Tyr Gln Pro Gly Thr  
 100 105 110  
 Leu Glu Ala Ile Ala Arg Asp Glu Ser Gly Lys Glu Ile Ala Arg Asp  
 115 120 125  
 Lys Ile Thr Thr Ala Gly Lys Pro Ala Ala Val Arg Leu Ile Lys Glu  
 130 135 140  
 Asp His Ala Ile Ala Ala Asp Gly Lys Asp Leu Thr Tyr Ile Tyr Tyr  
 145 150 155 160  
 Glu Ile Val Asp Ser Gln Gly Asn Val Val Pro Thr Ala Asn Asn Leu  
 165 170 175  
 Val Arg Phe Gln Leu His Gly Gln Gly Gln Leu Val Gly Val Asp Asn  
 180 185 190  
 Gly Glu Gln Ala Ser Arg Glu Arg Tyr Lys Ala Gln Ala Asp Gly Ser  
 195 200 205  
 Trp Ile Arg Lys Ala Phe Asn Gly Lys Gly Val Ala Ile Val Lys Ser  
 210 215 220  
 Thr Glu Gln Ala Gly Lys Phe Thr Leu Thr Ala His Ser Asp Leu Leu  
 225 230 235 240  
 Lys Ser Asn Gln Val Thr Val Phe Thr Gly Lys Lys Glu Gly Gln Glu  
 245 250 255  
 Lys Thr Val Leu Gly Thr Glu Val Pro Lys Val Gln Thr Ile Ile Gly  
 260 265 270  
 Glu Ala Pro Glu Met Pro Thr Thr Val Pro Phe Val Tyr Ser Asp Gly  
 275 280 285  
 Ser Arg Ala Glu Arg Pro Val Thr Trp Ser Ser Val Asp Val Ser Lys  
 290 295 300

Pro Gly Ile Val Thr Val Lys Gly Met Ala Asp Gly Arg Glu Val Glu  
 305 310 315 320  
 Ala Arg Val Glu Val Ile Ala Leu Lys Ser Glu Leu Pro Val Val Lys  
 325 330 335  
 Arg Ile Ala Pro Asn Thr Asp Leu Asn Ser Val Asp Lys Ser Val Ser  
 340 345 350  
 Tyr Val Leu Ile Asp Gly Ser Val Glu Glu Tyr Glu Val Asp Lys Trp  
 355 360 365  
 Glu Ile Ala Glu Glu Asp Lys Ala Lys Leu Ala Ile Pro Gly Ser Arg  
 370 375 380  
 Ile Gln Ala Thr Gly Tyr Leu Glu Gly Gln Pro Ile His Ala Thr Leu  
 385 390 395 400  
 Val Val Glu Glu Gly Asn Pro Ala Ala Pro Ala Val Pro Thr Val Thr  
 405 410 415  
 Val Gly Gly Glu Ala Val Thr Gly Leu Thr Ser Gln Lys Pro Met Gln  
 420 425 430  
 Tyr Arg Thr Leu Ala Tyr Gly Ala Lys Leu Pro Glu Val Thr Ala Ser  
 435 440 445  
 Ala Lys Asn Ala Ala Val Thr Val Leu Gln Ala Ser Ala Ala Asn Gly  
 450 455 460  
 Met Arg Ala Ser Ile Phe Ile Gln Pro Lys Asp Gly Gly Pro Leu Gln  
 465 470 475 480  
 Thr Tyr Ala Ile Gln Phe Leu Glu Glu Ala Pro Lys Ile Ala His Leu  
 485 490 495  
 Ser Leu Gln Val Glu Lys Ala Asp Ser Leu Lys Glu Asp Gln Thr Val  
 500 505 510  
 Lys Leu Ser Val Arg Ala His Tyr Gln Asp Gly Thr Gln Ala Val Leu  
 515 520 525  
 Pro Ala Asp Lys Val Thr Phe Ser Thr Ser Gly Glu Gly Glu Val Ala  
 530 535 540  
 Ile Arg Lys Gly Met Leu Glu Leu His Lys Pro Gly Ala Val Thr Leu  
 545 550 555 560  
 Asn Ala Glu Tyr Glu Gly Ala Lys Asp Gln Val Glu Leu Thr Ile Gln  
 565 570 575  
 Ala Asn Thr Glu Lys Lys Ile Ala Gln Ser Ile Arg Pro Val Asn Val  
 580 585 590  
 Val Thr Asp Leu His Gln Glu Pro Ser Leu Pro Ala Thr Val Thr Val  
 595 600 605  
 Glu Tyr Asp Lys Gly Phe Pro Lys Thr His Lys Val Thr Trp Gln Ala  
 610 615 620  
 Ile Pro Lys Glu Lys Leu Asp Ser Tyr Gln Thr Phe Glu Val Leu Gly  
 625 630 635 640  
 Lys Val Glu Gly Ile Asp Leu Glu Ala Arg Ala Lys Val Ser Val Glu

	645		650		655
Gly Ile Val Ser Val Glu Glu Val Ser Val Thr Thr Pro Ile Ala Glu	660		665		670
Ala Pro Gln Leu Pro Glu Ser Val Arg Thr Tyr Asp Ser Asn Gly His	675		680		685
Val Ser Ser Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr	690		695		700
Ala Lys Glu Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln	705		710		715
					720
Leu Thr					

## (2) INFORMATION FOR SEQ ID NO: 85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:



AGCTAAGGTT GCATGGGATG CGATTTCGTCC AGAGCAATAC GCTAAGGAAG GTGTC'TTTAC	60
AGTTAATGGT CGCTTAGAAG GTACGCAATT AACAACTAAA CTTTCATGTTT GCGTATCTGC	120
TCAAAC TGAG CAAGGTGCAA ACATTTCTGA CCAATGGACC GGTTTCAGAAT TGCCACTTGC	180
CTTTGCTTCA GACTCAAATC CAAGCGACCC AGTTTCAAAT GTTAATGACA AGCTCATTTT	240
CTACAATAAC CAACCAGCCA ATCGTTGGAC AAAC TGAAT CGTACTAATC CAGAAGCTTC	300
AGTCGGTGT CTGTTTGGAG ATTCAGGTAT CTTGAGCAAA CGCTCCGTTG ATAATCTAAG	360
TGTCGGATTC CATGAAGACC ATGGAGTTGG TGTACCGAAG TCTTATGTGA TTGAGTATTA	420
TGTTGGTAAG ACTGTCCCAA CAGCTCCTAA AAACCCTAGT TTTGTTGGTA ATGAGGACCA	480
TGTC'TTTAAT GATTCTGCCA ACTGGAAACC AGTTACTAAT CTAAAAGCCC CTGCTCAACT	540
CAAGGCTGGA GAAATGAACC ACTTTAGCTT TGATAAAGTT GAAACCTATG CTGTTCGTAT	600
TCGCATGGTT AAAGCAGATA ACAAGCGTGG AACGTCTATC ACAGAGGTAC AAATCTTTGC	660
GAAACAAGTT GCGGCAGCCA AGCAAGGACA AACAAGAATC CAAGTTGACG GCAAAGACTT	720
AGCAAAC'TTC AACCC'TGATT TGACAGACTA CTACCTTGAG TCTGTAGATG GAAAAGTTCC	780
GGCAGTCACA GCAAGTGTTA GCAACAATGG TCTCGCTACC GTCGTTCCAA GCGTTCGTGA	840
AGGTGAGCCA GTTCGTGTCA TCGCGAAAGC TGAAAATGGC GACATCTTAG GAGAATACCG	900
TCTGCACTTC ACTAAGGATA AGAGCTTACT TTCTCATAAA CCAGTTGCTG CGGTTAAACA	960
AGCTCGCTTG CTACAAGTAG GTCAAGCACT TGAATTGCCG ACTAAGGTTT CAGTTTACTT	1020
CACAGGTAAA GACGGCTACG AAACAAAAGA CCTGACAGTT GAATGGGAAG AAGTTCCAGC	1080



GGAAAATCTG ACAAAGCAG GTCAATTTAC TGTTCGAGGC CGTGTCCCTG GTAGTAACCT 1140  
 TGTTCGTGAG ATCACTGTAC GAGTGACAGA CAAACTTGGT GAGACTCTTT CAGATAACCC 1200  
 TAACTATGAT GAAAACAGTA ACCAGGCCCTT TGCTTCAGCA ACCAATGATA TTGACAAAAA 1260  
 CTCTCATGAC CGCGTTGACT ATCTCAATGA CGGAGATCAT TCAGAAAATC GTCGTTGGAC 1320  
 AAATGGTCA CCAACACCAT CTTCTAATCC AGAAGTATCA GCGGGTGTGA TTTTCCGTGA 1380  
 AAATGGTAAG ATTGTAGAAC GGACTGTTAC ACAAGGAAAA GTTCAGTTCT TTGCAGATAG 1440  
 TGGTACGGAT GCACCATCTA AACTCGTTTT AGAACGCTAT GTCGGTCCAG AGTTTGAAGT 1500  
 GCCAACCTAC TATTCAAACCT ACCAAGCCCTA CGACGCAGAC CATCCATTCA ACAATCCAGA 1560  
 AAATGGGAA GCTGTTCCCTT ATCGTGCGGA TAAAGACATT GCAGCTGGTG ATGAAATCAA 1620  
 CGTAACATTT AAAGCTATCA AAGCCAAAGC TATGAGATGG CGTATGGAGC GTAAAGCAGA 1680  
 TAAGAGCGGT GTTGCGATGA TTGAGATGAC CTTCCCTTGCA CCAAGTGAAT TGCCCAAGA 1740  
 AAGCACTCAA TCAAAGATTC TTGTAGATGG AAAAGAACTT GCTGATTTTCG CTGAAAATCG 1800  
 TCAAGACTAT CAAATTACCT ATAAAGGTCA ACGGCCAAAA GTCTCAGTTG AAGAAAACAA 1860  
 TCAAGTAGCT TCAACTGTGG TAGATAGTGG AGAAGATAGC TTTCCAGTAC TTGTTCCCTT 1920  
 CGTTTCAGAA AGTGGAAAAC AAGTCAAGGA ATACCGTATC CACTTGACTA AGGAAAAACC 1980  
 AGTTTCTGAG AAGACAGTTG CTGCTGTACA AGAAGATCTT CCAAAAATCG AATTTGTTGA 2040  
 AAAAGATTTG GCATACAAGA CAGTTGAGAA AAAAGATTCA ACACTGTATC TAGGTGAAAC 2100  
 TCGTGTAGAA CAAGAAGGAA AAGTTGAAA AGAACGTATC TTTACAGCGA TTAATCCTGA 2160  
 TGGAAGTAAG GAAGAAAAAC TCCGTGAAGT GGTAGAAGTT CCGACAGACC GCATCGTCTT 2220  
 GGTGGAACC AAACCAGTAG CTCAAGAAGC TAAAAACCA CAAGTGTGAG AAAAAGCAGA 2280  
 TACAAAACCA ATTGATTCAA GTGAAGCTAG TCAAATAAT AAAGCCCAG 2329

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr Ala Lys Glu  
 1 5 10 15  
 Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln Leu Thr Thr  
 20 25 30  
 Lys Leu His Val Arg Val Ser Ala Gln Thr Glu Gln Gly Ala Asn Ile  
 35 40 45

Ser Asp Gln Trp Thr Gly Ser Glu Leu Pro Leu Ala Phe Ala Ser Asp  
 50 55 60  
 Ser Asn Pro Ser Asp Pro Val Ser Asn Val Asn Asp Lys Leu Ile Ser  
 65 70 75 80  
 Tyr Asn Asn Gln Pro Ala Asn Arg Trp Thr Asn Trp Asn Arg Thr Asn  
 85 90 95  
 Pro Glu Ala Ser Val Gly Val Leu Phe Gly Asp Ser Gly Ile Leu Ser  
 100 105 110  
 Lys Arg Ser Val Asp Asn Leu Ser Val Gly Phe His Glu Asp His Gly  
 115 120 125  
 Val Gly Val Pro Lys Ser Tyr Val Ile Glu Tyr Tyr Val Gly Lys Thr  
 130 135 140  
 Val Pro Thr Ala Pro Lys Asn Pro Ser Phe Val Gly Asn Glu Asp His  
 145 150 155 160  
 Val Phe Asn Asp Ser Ala Asn Trp Lys Pro Val Thr Asn Leu Lys Ala  
 165 170 175  
 Pro Ala Gln Leu Lys Ala Gly Glu Met Asn His Phe Ser Phe Asp Lys  
 180 185 190  
 Val Glu Thr Tyr Ala Val Arg Ile Arg Met Val Lys Ala Asp Asn Lys  
 195 200 205  
 Arg Gly Thr Ser Ile Thr Glu Val Gln Ile Phe Ala Lys Gln Val Ala  
 210 215 220  
 Ala Ala Lys Gln Gly Gln Thr Arg Ile Gln Val Asp Gly Lys Asp Leu  
 225 230 235 240  
 Ala Asn Phe Asn Pro Asp Leu Thr Asp Tyr Tyr Leu Glu Ser Val Asp  
 245 250 255  
 Gly Lys Val Pro Ala Val Thr Ala Ser Val Ser Asn Asn Gly Leu Ala  
 260 265 270  
 Thr Val Val Pro Ser Val Arg Glu Gly Glu Pro Val Arg Val Ile Ala  
 275 280 285  
 Lys Ala Glu Asn Gly Asp Ile Leu Gly Glu Tyr Arg Leu His Phe Thr  
 290 295 300  
 Lys Asp Lys Ser Leu Leu Ser His Lys Pro Val Ala Ala Val Lys Gln  
 305 310 315 320  
 Ala Arg Leu Leu Gln Val Gly Gln Ala Leu Glu Leu Pro Thr Lys Val  
 325 330 335  
 Pro Val Tyr Phe Thr Gly Lys Asp Gly Tyr Glu Thr Lys Asp Leu Thr  
 340 345 350  
 Val Glu Trp Glu Glu Val Pro Ala Glu Asn Leu Thr Lys Ala Gly Gln  
 355 360 365  
 Phe Thr Val Arg Gly Arg Val Leu Gly Ser Asn Leu Val Ala Glu Ile  
 370 375 380

Thr Val Arg Val Thr Asp Lys Leu Gly Glu Thr Leu Ser Asp Asn Pro  
 385 390 395 400  
 Asn Tyr Asp Glu Asn Ser Asn Gln Ala Phe Ala Ser Ala Thr Asn Asp  
 405 410 415  
 Ile Asp Lys Asn Ser His Asp Arg Val Asp Tyr Leu Asn Asp Gly Asp  
 420 425 430  
 His Ser Glu Asn Arg Arg Trp Thr Asn Trp Ser Pro Thr Pro Ser Ser  
 435 440 445  
 Asn Pro Glu Val Ser Ala Gly Val Ile Phe Arg Glu Asn Gly Lys Ile  
 450 455 460  
 Val Glu Arg Thr Val Thr Gln Gly Lys Val Gln Phe Phe Ala Asp Ser  
 465 470 475 480  
 Gly Thr Asp Ala Pro Ser Lys Leu Val Leu Glu Arg Tyr Val Gly Pro  
 485 490 495  
 Glu Phe Glu Val Pro Thr Tyr Tyr Ser Asn Tyr Gln Ala Tyr Asp Ala  
 500 505 510  
 Asp His Pro Phe Asn Asn Pro Glu Asn Trp Glu Ala Val Pro Tyr Arg  
 515 520 525  
 Ala Asp Lys Asp Ile Ala Ala Gly Asp Glu Ile Asn Val Thr Phe Lys  
 530 535 540  
 Ala Ile Lys Ala Lys Ala Met Arg Trp Arg Met Glu Arg Lys Ala Asp  
 545 550 555 560  
 Lys Ser Gly Val Ala Met Ile Glu Met Thr Phe Leu Ala Pro Ser Glu  
 565 570 575  
 Leu Pro Gln Glu Ser Thr Gln Ser Lys Ile Leu Val Asp Gly Lys Glu  
 580 585 590  
 Leu Ala Asp Phe Ala Glu Asn Arg Gln Asp Tyr Gln Ile Thr Tyr Lys  
 595 600 605  
 Gly Gln Arg Pro Lys Val Ser Val Glu Glu Asn Asn Gln Val Ala Ser  
 610 615 620  
 Thr Val Val Asp Ser Gly Glu Asp Ser Phe Pro Val Leu Val Arg Leu  
 625 630 635 640  
 Val Ser Glu Ser Gly Lys Gln Val Lys Glu Tyr Arg Ile His Leu Thr  
 645 650 655  
 Lys Glu Lys Pro Val Ser Glu Lys Thr Val Ala Ala Val Gln Glu Asp  
 660 665 670  
 Leu Pro Lys Ile Glu Phe Val Glu Lys Asp Leu Ala Tyr Lys Thr Val  
 675 680 685  
 Glu Lys Lys Asp Ser Thr Leu Tyr Leu Gly Glu Thr Arg Val Glu Gln  
 690 695 700  
 Glu Gly Lys Val Gly Lys Glu Arg Ile Phe Thr Ala Ile Asn Pro Asp  
 705 710 715 720  
 Gly Ser Lys Glu Glu Lys Leu Arg Glu Val Val Glu Val Pro Thr Asp

	725		730		735
Arg Ile Val Leu Val Gly Thr Lys Pro Val Ala Gln Glu Ala Lys Lys					
	740		745		750
Pro Gln Val Ser Glu Lys Ala Asp Thr Lys Pro Ile Asp Ser Ser Glu					
	755		760		765
Ala Ser Gln Thr Asn Lys Ala Gln					
	770		775		

## (2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CTATCACTAT GTAAATAAAG AGATTATTTT ACAAGAAGCT AAAGATTTAA TTCAGACAGG	60
AAAGCCTGAC AGGAATGAAG TTGTATATGG TTTGGTGTAT CAAAAGATC AGTTGCCTCA	120
AACAGGGACA GAA	133

## (2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 44 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Tyr His Tyr Val Asn Lys Glu Ile Ile Ser Gln Glu Ala Lys Asp Leu	
1	5 10 15
Ile Gln Thr Gly Lys Pro Asp Arg Asn Glu Val Val Tyr Gly Leu Val	
	20 25 30
Tyr Gln Lys Asp Gln Leu Pro Gln Thr Gly Thr Glu	
	35 40

## (2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 775 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TGAGACTCCT CAATCAATAA CAAATCAGGA GCAAGCTAGG ACAGAAAACC AAGTAGTAGA	60
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GACAGAGGAA GCTCCAAAAG AAGAAGCACC TAAAACAGAA GAAAGTCCAA AGGAAGAACC 120  
 AAAATCGGAG GTAAAACCTA CTGACGACAC CCTTCCTAAA GTAGAAGAGG GGAAAGAAGA 180  
 TTCAGCAGAA CCAGCTCCAG TTGAAGAAGT AGGTGGAGAA GTTGAGTCAA AACCAGAGGA 240  
 AAAAGTAGCA GTTAAGCCAG AAAGTCAACC ATCAGACAAA CCAGCTGAGG AATCAAAAGT 300  
 TGAACAAGCA GGTGAACCAG TCGCGCCAAG AGAAGACGAA AAGGCACCAG TCGAGCCAGA 360  
 AAAGCAACCA GAAGCTCCTG AAGAAGAGAA GGCTGTAGAG GAAACACCGA AACAAGAAGA 420  
 GTCAACTCCA GATACCAAGG CTGAAGAAAC TGTAGAACCA AAAGAGGAGA CTGTTAATCA 480  
 ATCTATTGAA CAACCAAAAG TTGAAACGCC TGCTGTAGAA AAACAAACAG AACCAACAGA 540  
 GGAACCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AACAGGCACC 600  
 AACGGCACCA GTTGAGCCAG AAAAGCAACC AGAAGTTCCT GAAGAAGAGA AGGCTGTAGA 660  
 GGAAACACCG AAACCAGAAG ATAAAATAAA GGGTATTGGT ACTAAAGAAC CAGTTGATAA 720  
 AAGTGAGTTA AATAATCAAA TTGATAAAGC TAGTTCAGTT TCTCCTACTG ATTAT 775

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Glu Thr Pro Gln Ser Ile Thr Asn Gln Glu Gln Ala Arg Thr Glu Asn  
 1 5 10 15  
 Gln Val Val Glu Thr Glu Glu Ala Pro Lys Glu Glu Ala Pro Lys Thr  
 20 25 30  
 Glu Glu Ser Pro Lys Glu Glu Pro Lys Ser Glu Val Lys Pro Thr Asp  
 35 40 45  
 Asp Thr Leu Pro Lys Val Glu Glu Gly Lys Glu Asp Ser Ala Glu Pro  
 50 55 60  
 Ala Pro Val Glu Glu Val Gly Gly Glu Val Glu Ser Lys Pro Glu Glu  
 65 70 75 80  
 Lys Val Ala Val Lys Pro Glu Ser Gln Pro Ser Asp Lys Pro Ala Glu  
 85 90 95  
 Glu Ser Lys Val Glu Gln Ala Gly Glu Pro Val Ala Pro Arg Glu Asp  
 100 105 110  
 Glu Lys Ala Pro Val Glu Pro Glu Lys Gln Pro Glu Ala Pro Glu Glu  
 115 120 125  
 Glu Lys Ala Val Glu Glu Thr Pro Lys Gln Glu Glu Ser Thr Pro Asp  
 130 135 140

Thr Lys Ala Glu Glu Thr Val Glu Pro Lys Glu Glu Thr Val Asn Gln  
 145 150 155 160  
 Ser Ile Glu Gln Pro Lys Val Glu Thr Pro Ala Val Glu Lys Gln Thr  
 165 170 175  
 Glu Pro Thr Glu Glu Pro Lys Val Glu Gln Ala Gly Glu Pro Val Ala  
 180 185 190  
 Pro Arg Glu Asp Glu Gln Ala Pro Thr Ala Pro Val Glu Pro Glu Lys  
 195 200 205  
 Gln Pro Glu Val Pro Glu Glu Lys Ala Val Glu Glu Thr Pro Lys  
 210 215 220  
 Pro Glu Asp Lys Ile Lys Gly Ile Gly Thr Lys Glu Pro Val Asp Lys  
 225 230 235 240  
 Ser Glu Leu Asn Asn Gln Ile Asp Lys Ala Ser Ser Val Ser Pro Thr  
 245 250 255  
 Asp Tyr

## (2) INFORMATION FOR SEQ ID NO: 91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

GGATGCTCAA GAAACTGCGG GAGTTCAC TA AATATGTG GCAGATTCAG AGCTATCATC 60  
 AGAAGAAAAG AAGCAGCTTG TCTATGATAT TCCGACATAC GTGGAGAATG ATGATGAAAC 120  
 TTATTATCTT GTTTATAAGT TAAATTCTCA AAATCAACTG GCGGAATTGC CAAATACTGG 180  
 AAGCAAGAAT GAGAGGCAA 199

## (2) INFORMATION FOR SEQ ID NO:92:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Asp Ala Gln Glu Thr Ala Gly Val His Tyr Lys Tyr Val Ala Asp Ser  
 1 5 10 15  
 Glu Leu Ser Ser Glu Glu Lys Lys Gln Leu Val Tyr Asp Ile Pro Thr  
 20 25 30

Tyr Val Glu Asn Asp Asp Glu Thr Tyr Tyr Leu Val Tyr Lys Leu Asn  
35 40 45

Ser Gln Asn Gln Leu Ala Glu Leu Pro Asn Thr Gly Ser Lys Asn Glu  
50 55 60

Arg Gln  
65

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CGACAAAGGT GAGACTGAGG TTCAACCAGA GTCGCCAGAT ACTGTGGTAA GTGATAAAGG 60  
TGAACCAGAG CAGGTAGCAC CGCTTCCAGA ATATAAGGGT AATATTGAGC AAGTAAAACC 120  
TGAAACTCCG GTTGAGAAGA CCAAAGAACA AGGTCCAGAA AAAACTGAAG AAGTTCCAGT 180  
AAAACCAACA GAAGAAACAC CAGTAAATCC AAATGAAGGT ACTACAGAAG GAACCTCAAT 240  
TCAAGAAGCA GAAAATCCAG TTCAACCTGC AGAAGAATCA ACAACGAATT CAGAGAAAGT 300  
ATCACCAGAT ACATCTAGCA AAAATACTGG GGAAGTGTCC AGTAATCCTA GTGATTTCGAC 360  
AACCTCAGTT GGAGAATCAA ATAAACCAGA ACATAATGAC TCTAAAAATG AAAATTCAGA 420  
AAAAACTGTA GAAGAAGTTC CAGTAAATCC AAATGAAGGC ACAGTAGAAG GTACCTCAAA 480  
TCAAGAAACA GAAAAACCAG TTCAACCTGC AGAAGAAACA CAAACAAACT CTGGGAAAAT 540  
AGCTAACGAA AATACTGGAG AAGTATCCAA TAAACCTAGT GATTCAAAAC CACCAGTTGA 600  
AGAATCAAAT CAACCAGAAA AAAACGGAAC TGCAACAAAA CCAGAAAATT CAGGTAATAC 660  
AACATCAGAG AATGGACAAA CAGAACCAGA ACCATCAAAC GGAAATTCAA CTGAGGATGT 720  
TTCAACCGAA TCAAACACAT CCAATTCAAA TGGAACGAA GAAATTAAAC AAGAAAATGA 780  
ACTAGACCCT GATAAAAAGG TAGAAGAACC AGAGAAAACA CTTGAATTAA GAAAT 835

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp Lys Gly Glu Thr Glu Val Gln Pro Glu Ser Pro Asp Thr Val Val  
1 5 10 15

Ser Asp Lys Gly Glu Pro Glu Gln Val Ala Pro Leu Pro Glu Tyr Lys  
 20 25 30  
 Gly Asn Ile Glu Gln Val Lys Pro Glu Thr Pro Val Glu Lys Thr Lys  
 35 40 45  
 Glu Gln Gly Pro Glu Lys Thr Glu Glu Val Pro Val Lys Pro Thr Glu  
 50 55 60  
 Glu Thr Pro Val Asn Pro Asn Glu Gly Thr Thr Glu Gly Thr Ser Ile  
 65 70 75 80  
 Gln Glu Ala Glu Asn Pro Val Gln Pro Ala Glu Glu Ser Thr Thr Asn  
 85 90 95  
 Ser Glu Lys Val Ser Pro Asp Thr Ser Ser Lys Asn Thr Gly Glu Val  
 100 105 110  
 Ser Ser Asn Pro Ser Asp Ser Thr Thr Ser Val Gly Glu Ser Asn Lys  
 115 120 125  
 Pro Glu His Asn Asp Ser Lys Asn Glu Asn Ser Glu Lys Thr Val Glu  
 130 135 140  
 Glu Val Pro Val Asn Pro Asn Glu Gly Thr Val Glu Gly Thr Ser Asn  
 145 150 155 160  
 Gln Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn  
 165 170 175  
 Ser Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro  
 180 185 190  
 Ser Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn  
 195 200 205  
 Gly Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn  
 210 215 220  
 Gly Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val  
 225 230 235 240  
 Ser Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys  
 245 250 255  
 Gln Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys  
 260 265 270  
 Thr Leu Glu Leu Arg Asn  
 275

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:



AAATCAATTG GTAGCACAAG ATCCAAAAGC ACAAGATAGC ACTAAACTGA CTGCTGAAAA 60  
 ATCAACTGTT AAAGCACCTG CTCAAAGAGT AGATGTAAAA GATATAACTC ATTTAACAGA 120  
 TGAAGAAAAA GTTAAGGTTG CTATTTTACA AGCAAATGGT TCAGCATTAG ACGGAGCGAC 180  
 AATCAATGTA GCTGGAGATG GTACAGCAAC AATCACATTC CCAGATGGTT CAGTAGTGAC 240  
 GATTCTAGGA AAAGATACAG TTCAACAATC TGCAGAAAGGT GAATCTGTAA CTCAAGAAGC 300  
 TACACCAGAG TATAAGCTAG AAAATACACC AGGTGGAGAT AAGGGAGGCA ATACTGGAAG 360  
 CTCAGATGCT AATGCGAATG AAGGCGGTGG TAGCCAGGCG GGTGGATCAG CTCACACAGG 420  
 TTCACAAAAC TCAGCTCAAT CACAAGCTTC TAAGCAATTA GCTACTGAAA AAGAATCAGC 480  
 TAAAAATGCC ATTGAAAAAG CAGCCAAGGA CAAGCAGGAT GAAATCAAAG GCGCACCGCT 540  
 TTCTGATAAA GAAAAAGCAG AACTTTTAGC AAGAGTGGA GAGAAAAAC AAGCAGCTCT 600  
 CAAAGAGATT GAAATGCGA AACTATGGA AGATGTGAAG GAAGCAGAAA CGATTGGAGT 660  
 GCAAGCCATT GCCATGGTTA CAGTTCCTAA GAGACCAGTG GCTCCTAAT 709

## (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 236 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Asn Gln Leu Val Ala Gln Asp Pro Lys Ala Gln Asp Ser Thr Lys Leu  
 1 5 10 15  
 Thr Ala Glu Lys Ser Thr Val Lys Ala Pro Ala Gln Arg Val Asp Val  
 20 25 30  
 Lys Asp Ile Thr His Leu Thr Asp Glu Glu Lys Val Lys Val Ala Ile  
 35 40 45  
 Leu Gln Ala Asn Gly Ser Ala Leu Asp Gly Ala Thr Ile Asn Val Ala  
 50 55 60  
 Gly Asp Gly Thr Ala Thr Ile Thr Phe Pro Asp Gly Ser Val Val Thr  
 65 70 75 80  
 Ile Leu Gly Lys Asp Thr Val Gln Gln Ser Ala Lys Gly Glu Ser Val  
 85 90 95  
 Thr Gln Glu Ala Thr Pro Glu Tyr Lys Leu Glu Asn Thr Pro Gly Gly  
 100 105 110  
 Asp Lys Gly Gly Asn Thr Gly Ser Ser Asp Ala Asn Ala Asn Glu Gly  
 115 120 125  
 Gly Gly Ser Gln Ala Gly Gly Ser Ala His Thr Gly Ser Gln Asn Ser  
 130 135 140

Ala Gln Ser Gln Ala Ser Lys Gln Leu Ala Thr Glu Lys Glu Ser Ala  
 145 150 155 160

Lys Asn Ala Ile Glu Lys Ala Ala Lys Asp Lys Gln Asp Glu Ile Lys  
 165 170 175

Gly Ala Pro Leu Ser Asp Lys Glu Lys Ala Glu Leu Leu Ala Arg Val  
 180 185 190

Glu Ala Glu Lys Gln Ala Ala Leu Lys Glu Ile Glu Asn Ala Lys Thr  
 195 200 205

Met Glu Asp Val Lys Glu Ala Glu Thr Ile Gly Val Gln Ala Ile Ala  
 210 215 220

Met Val Thr Val Pro Lys Arg Pro Val Ala Pro Asn  
 225 230 235

## (2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 787 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CAAACAGTCA GCTTCAGGAA CGATTGAGGT GATTTCACGA GAAAATGGCT CTGGGACACG 60

GGGTGCCTTC ACAGAAATCA CAGGGATTCT CAAAAAGAC GGTGATAAAA AAATTGACAA 120

CACTGCCAAA ACAGCTGTGA TTCAAAATAG TACAGAAGGT GTTCTCTCAG CAGTTCAAGG 180

GAATGCTAAT GCTATCGGCT ACATCTCCTT GGGATCTTTA ACGAAATCTG TCAAGGCTTT 240

AGAGATTGAT GGTGTCAAGG CTAGTCGAGA CACAGTTTTA GATGGTGAAT ACCCTCTTCA 300

ACGTCCCTTC AACATTGTTT GGTCTTCTAA TCTTTCCAAG CTAGGTCAAG ATTTTATCAG 360

CTTTATCCAC TCCAAACAAG GTCAACAAGT GGTCACAGAT AATAAATTTA TTGAAGCTAA 420

AACCGAAACC ACGGAATATA CAAGCCAACA CTTATCAGGC AAGTTGTCTG TTGTAGGTTT 480

CACTTCAGTA TCTTCTTTAA TGGAAAAATT AGCAGAAGCT TATAAAAAAG AAAATCCAGA 540

AGTTACGATT GATATTACCT CTAATGGGTC TTCAGCAGGT ATTACCGCTG TTAAGGAGAA 600

AACCGCTGAT ATTGGTATGG TTTCTAGGGA ATTAACCTCT GAAGAAGGTA AGAGTCTCAC 660

CCATGATGCT ATTGCTTTAG ACGGTATTGC TGTGTGGTTC AATAATGACA ATAAGGCAAG 720

CCAAGTCAGT ATGGCTGAAC TTGCAGACGT TTTTAGTGGC AAATTAACCA CCTGGGACAA 780

GATTAAA 787


## (2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 262 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:



Lys Gln Ser Ala Ser Gly Thr Ile Glu Val Ile Ser Arg Glu Asn Gly  
 1 5 10 15  
 Ser Gly Thr Arg Gly Ala Phe Thr Glu Ile Thr Gly Ile Leu Lys Lys  
 20 25 30  
 Asp Gly Asp Lys Lys Ile Asp Asn Thr Ala Lys Thr Ala Val Ile Gln  
 35 40 45  
 Asn Ser Thr Glu Gly Val Leu Ser Ala Val Gln Gly Asn Ala Asn Ala  
 50 55 60  
 Ile Gly Tyr Ile Ser Leu Gly Ser Leu Thr Lys Ser Val Lys Ala Leu  
 65 70 75 80  
 Glu Ile Asp Gly Val Lys Ala Ser Arg Asp Thr Val Leu Asp Gly Glu  
 85 90 95  
 Tyr Pro Leu Gln Arg Pro Phe Asn Ile Val Trp Ser Ser Asn Leu Ser  
 100 105 110  
 Lys Leu Gly Gln Asp Phe Ile Ser Phe Ile His Ser Lys Gln Gly Gln  
 115 120 125  
 Gln Val Val Thr Asp Asn Lys Phe Ile Glu Ala Lys Thr Glu Thr Thr  
 130 135 140  
 Glu Tyr Thr Ser Gln His Leu Ser Gly Lys Leu Ser Val Val Gly Ser  
 145 150 155 160  
 Thr Ser Val Ser Ser Leu Met Glu Lys Leu Ala Glu Ala Tyr Lys Lys  
 165 170 175  
 Glu Asn Pro Glu Val Thr Ile Asp Ile Thr Ser Asn Gly Ser Ser Ala  
 180 185 190  
 Gly Ile Thr Ala Val Lys Glu Lys Thr Ala Asp Ile Gly Met Val Ser  
 195 200 205  
 Arg Glu Leu Thr Pro Glu Glu Gly Lys Ser Leu Thr His Asp Ala Ile  
 210 215 220  
 Ala Leu Asp Gly Ile Ala Val Val Val Asn Asn Asp Asn Lys Ala Ser  
 225 230 235 240  
 Gln Val Ser Met Ala Glu Leu Ala Asp Val Phe Ser Gly Lys Leu Thr  
 245 250 255  
 Thr Trp Asp Lys Ile Lys  
 260

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ATTCGATGAT GCGGATGAAA AGATGACCCG TGATGAAATT GCCTATATGC TGACAAATAG 60  
 TGAAGAAACA TTGGATGCTG ATGAGATTGA GATGCTACAA GGTGTCTTTT CGCTCGATGA 120  
 ACTGATGGCA CGAGAGGTTA TGGTTCCTCG AACGGATGCC TTTATGGTGG ATATTCAGGA 180  
 TGATAGTCAA GCCATTATCC AAAGTATTTT AAAACAAAAT TATTCTCGTA TCCCGGTTTA 240  
 TGATGGGGAT AAGGACAATG TAATTGGAAT CATTCACACC AAGAGTCTCC TTAAGGCAGG 300  
 CTTTGTGGAC GGTTTTGACA ATATTGTTTG GAAGAGAATT TTACAAGATC CACTTTTTGT 360  
 ACCTGAAACT ATTTTTGTGG ATGACTTGCT AAAAGAACTG CGAAATACCC AAAGACAAAT 420  
 G 421


(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:



Phe Asp Asp Ala Asp Glu Lys Met Thr Arg Asp Glu Ile Ala Tyr Met  
 1 5 10 15  
 Leu Thr Asn Ser Glu Glu Thr Leu Asp Ala Asp Glu Ile Glu Met Leu  
 20 25 30  
 Gln Gly Val Phe Ser Leu Asp Glu Leu Met Ala Arg Glu Val Met Val  
 35 40 45  
 Pro Arg Thr Asp Ala Phe Met Val Asp Ile Gln Asp Asp Ser Gln Ala  
 50 55 60  
 Ile Ile Gln Ser Ile Leu Lys Gln Asn Tyr Ser Arg Ile Pro Val Tyr  
 65 70 75 80  
 Asp Gly Asp Lys Asp Asn Val Ile Gly Ile Ile His Thr Lys Ser Leu  
 85 90 95  
 Leu Lys Ala Gly Phe Val Asp Gly Phe Asp Asn Ile Val Trp Lys Arg  
 100 105 110  
 Ile Leu Gln Asp Pro Leu Phe Val Pro Glu Thr Ile Phe Val Asp Asp  
 115 120 125  
 Leu Leu Lys Glu Leu Arg Asn Thr Gln Arg Gln Met  
 130 135 140

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```


GGAGAGTCGA TCAAAAGTAG ATGAAGCTGT GTCTAAGTTT GAAAAGGACT CATCTTCTTC      60
GTCAAGTTCA GACTCTTCCA CTAAACCGGA AGCTTCAGAT ACAGCGAAGC CAAACAAGCC      120
GACAGAACCA GGAGAAAAGG TAGCAGAAGC TAAGAAGAAG GTTGAAGAAG CTGAGAAAAA      180
AGCCAAGGAT CAAAAAGAAG AAGATCGTCG TAACTACCCA ACCATTACTT ACAAACGCT      240
TGAACCTGAA ATTGCTGAGT CCGATGTGGA AGTTAAAAAA GCGGAGCTTG AACTAGTAAA      300
AGTGAAAGCT AACGAACCTC GAGACGAGCA A                                     331
  
```

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 110 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:



```

Glu Ser Arg Ser Lys Val Asp Glu Ala Val Ser Lys Phe Glu Lys Asp
1           5           10
Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Lys Pro Glu Ala Ser
20          25          30
Asp Thr Ala Lys Pro Asn Lys Pro Thr Glu Pro Gly Glu Lys Val Ala
35          40          45
Glu Ala Lys Lys Lys Val Glu Glu Ala Glu Lys Lys Ala Lys Asp Gln
50          55          60
Lys Glu Glu Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys Thr Leu
65          70          75          80
Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu
85          90          95
Glu Leu Val Lys Val Lys Ala Asn Glu Pro Arg Asp Glu Gln
100         105         110
  
```

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

ATGGACAACA GGAAACTGGG ACGAGGTTAT ATCTGGTAAG ATTGACAAGT ACAAAGATCC	60
AGATATTCCA ACAGTTGAAT CACAAGAAGT TACGTCAGAC TCTAGTGATA AAGAAATAAC	120
GGTAAGGTAT GACCGTTTAT CAACACCAGA AAAACCAATC CCACAACCAA ATCCAGAGCA	180
TCCAAGTGTT CCGACACCAA ACCCAGAACT ACCAAATCAA GAGACTCCAA CACCAGATAA	240
ACCAACTCCA GAACCAGGTA CTCCAAAAAC TGAAACTCCA GTGAATCCAG ACCCAGAAGT	300
TCCGACTTAT GAGACAGGTA AGAGAGAGGA ATTGCCAAAC ACAGGTACAG AAGCTAAT	358


(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:



Trp	Thr	Thr	Gly	Asn	Trp	Asp	Glu	Val	Ile	Ser	Gly	Lys	Ile	Asp	Lys	1	5	10	15
Tyr	Lys	Asp	Pro	Asp	Ile	Pro	Thr	Val	Glu	Ser	Gln	Glu	Val	Thr	Ser	20	25	30	
Asp	Ser	Ser	Asp	Lys	Glu	Ile	Thr	Val	Arg	Tyr	Asp	Arg	Leu	Ser	Thr	35	40	45	
Pro	Glu	Lys	Pro	Ile	Pro	Gln	Pro	Asn	Pro	Glu	His	Pro	Ser	Val	Pro	50	55	60	
Thr	Pro	Asn	Pro	Glu	Leu	Pro	Asn	Gln	Glu	Thr	Pro	Thr	Pro	Asp	Lys	65	70	75	80
Pro	Thr	Pro	Glu	Pro	Gly	Thr	Pro	Lys	Thr	Glu	Thr	Pro	Val	Asn	Pro	85	90	95	
Asp	Pro	Glu	Val	Pro	Thr	Tyr	Glu	Thr	Gly	Lys	Arg	Glu	Glu	Leu	Pro	100	105	110	
Asn	Thr	Gly	Thr	Glu	Ala	Asn										115			

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CGATGGGCTC AATCCAACCC CAGGTCAAGT CTTACCTGAA GAGACATCGG GAACGAAAGA 60

GGGTGACTTA TCAGAAAAAC CAGGAGACAC CGTTCTCACT CAAGCGAAAC CTGAGGGCGT 120

TACTGGAAAT ACGAATTCAC TTCCGACACC TACAGAAAGA ACTGAAGTGA GCGAGGAAAC 180

AAGCCCTTCT AGTCTGGATA CACTTTTTTGA AAAAGATGAA GAAGCTCAAA AAAATCCAGA 240

GCTAACAGAT GTCTTAAAAG AAAGTGTAGA TACAGCTGAT GTGGATGGGA CACAAGCAAG 300

TCCAGCAGAA ACTACTCCTG AACAAAGTAA AGGTGGAGTG AAAGAAAATA CAAAAGACAG 360

CATCGATGTT CCTGCTGCTT ATCTTGAAAA AGCTGAAGGG AAAGGTCCTT TCACTGCCGG 420

TGTAAACCAA GTAATTCCTT ATGAACATT CGCTGGTGAT GGTATGTTAA CTCGCTATT 480

ACTAAAAGCT TCGGATAATG CTCCTTGGTC TGACAATGGT ACTGCTAAAA ATCCTGCTTT 540

ACCTCCTCTT GAAGGATTAA CAAAAGGGAA ATACTTCTAT GAAGTAGACT TAAATGGCAA 600

TACTGTTGGT AAACAAGGTC AAGCTTTAAT TGATCAACTT CGCGCTAATG GTACTCAAAC 660

TTATAAAGCT ACTGTTAAAG TTTACGGAAA TAAAGACGGT AAAGCTGACT TGACTAATCT 720

AGTTGCTACT AAAAATGTAG ACATCAACAT CAATGGATTA GTTGCTAAAG AAACAGTTCA 780

AAAAGCCGTT GCAGACAACG TTAAAGACAG TATCGATGTT CCAGCAGCCT ACCTAGAAAA 840

AGCCAAGGGT GAAGGTCCAT TCACAGCAGG TGTCAACCAT GTGATTCCAT ACGAACTCTT 900

CGCAGGTGAT GGCATGTTGA CTCGTCTCTT GCTCAAGGCA TCTGACAAGG CACCATGGTC 960

AGATAACGGC GACGCTAAAA ACCCAGCCCCT ATCTCCACTA GGCGAAAACG TGAAGACCAA 1020

AGGTCAATAC TTCTATCAAN TAGCCTTGGA CGGAAATGTA GCTGGCAAAG AAAACAAGC 1080

GCTCATTGAC CAGTTCCGAG CAAANGGTAC TCAAACCTAC AGCGCTACAG TCAATGTCTA 1140

TGGTAACAAA GACGGTAAAC CAGACTTGGA CAACATCGTA GCAACTAAAA AAGTCACTAT 1200

TAACATAAAC GGTTTAATTT CTAAAGAAAC AGTTCAAAAA GCCGTTGCAG ACAACGTTAA 1260

NGACAGTATC GATGTTCCAG CAGCCTACCT AGAAAAAGCC AAGGGTGAAG GTCCATTAC 1320

AGCAGGTGTC AACCATGTGA TTCCATACGA ACTCTTCGCA GGTGATGGTA TGTGACTCG 1380

TCTCTTGCTC AAGGCATCTG ACAAGGCACC ATGGTCAGAT AACGGNGACG CTAAAAACCC 1440

AGCNCTATCT CCACTAGGTG AAAACGTGAA GACCAGAGGT CAATACTTCT ATCAANTAGC 1500

CTTGACCGA AATGTAGCTG GCAAAGAAAA ACAAGCGCTC ATTGACCAGT TCCGAGCAAA 1560

CGGTACTCAA ACTTACAGCG CTACAGTCAA TGTCTATGGT AACAAAGACG GTAAACCAGA 1620

CTTGACAAC ATCGTAGCAA CTAAAAAGT CACTATTAAG ATAAATGTTA AAGAAACATC 1680

AGACACAGCA AATGGTTCAT TATCACCTTC TAACTCTGGT TCTGGCGTGA CTCCGATGAA 1740

TCACAATCAT GCTACAGGTA CTACAGATAG CATGCCTGCT GACACCATGA CAAGTTCTAC 1800

CAACACGATG GCAGGTGAAA ACATGGCTGC TTCTGCTAAC AAGATGTCTG ATACGATGAT 1860

GTCAGAGGAT AAAGCTATG 1879

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Asp Gly Leu Asn Pro Thr Pro Gly Gln Val Leu Pro Glu Glu Thr Ser  
 1 5 10 15  
 Gly Thr Lys Glu Gly Asp Leu Ser Glu Lys Pro Gly Asp Thr Val Leu  
 20 25 30  
 Thr Gln Ala Lys Pro Glu Gly Val Thr Gly Asn Thr Asn Ser Leu Pro  
 35 40 45  
 Thr Pro Thr Glu Arg Thr Glu Val Ser Glu Glu Thr Ser Pro Ser Ser  
 50 55 60  
 Leu Asp Thr Leu Phe Glu Lys Asp Glu Glu Ala Gln Lys Asn Pro Glu  
 65 70 75 80  
 Leu Thr Asp Val Leu Lys Glu Thr Val Asp Thr Ala Asp Val Asp Gly  
 85 90 95  
 Thr Gln Ala Ser Pro Ala Glu Thr Thr Pro Glu Gln Val Lys Gly Gly  
 100 105 110  
 Val Lys Glu Asn Thr Lys Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu  
 115 120 125  
 Glu Lys Ala Glu Gly Lys Gly Pro Phe Thr Ala Gly Val Asn Gln Val  
 130 135 140  
 Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu  
 145 150 155 160  
 Leu Lys Ala Ser Asp Asn Ala Pro Trp Ser Asp Asn Gly Thr Ala Lys  
 165 170 175  
 Asn Pro Ala Leu Pro Pro Leu Glu Gly Leu Thr Lys Gly Lys Tyr Phe  
 180 185 190  
 Tyr Glu Val Asp Leu Asn Gly Asn Thr Val Gly Lys Gln Gly Gln Ala  
 195 200 205  
 Leu Ile Asp Gln Leu Arg Ala Asn Gly Thr Gln Thr Tyr Lys Ala Thr  
 210 215 220  
 Val Lys Val Tyr Gly Asn Lys Asp Gly Lys Ala Asp Leu Thr Asn Leu  
 225 230 235 240  
 Val Ala Thr Lys Asn Val Asp Ile Asn Ile Asn Gly Leu Val Ala Lys  
 245 250 255  
 Glu Thr Val Gln Lys Ala Val Ala Asp Asn Val Lys Asp Ser Ile Asp  
 260 265 270



Val Pro Ala Ala Tyr Leu Glu Lys Ala Lys Gly Glu Gly Pro Phe Thr  
 275 280 285  
 Ala Gly Val Asn His Val Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly  
 290 295 300  
 Met Leu Thr Arg Leu Leu Leu Lys Ala Ser Asp Lys Ala Pro Trp Ser  
 305 310 315 320  
 Asp Asn Gly Asp Ala Lys Asn Pro Ala Leu Ser Pro Leu Gly Glu Asn  
 325 330 335  
 Val Lys Thr Lys Gly Gln Tyr Phe Tyr Gln Xaa Ala Leu Asp Gly Asn  
 340 345 350  
 Val Ala Gly Lys Glu Lys Gln Ala Leu Ile Asp Gln Phe Arg Ala Xaa  
 355 360 365  
 Gly Thr Gln Thr Tyr Ser Ala Thr Val Asn Val Tyr Gly Asn Lys Asp  
 370 375 380  
 Gly Lys Pro Asp Leu Asp Asn Ile Val Ala Thr Lys Lys Val Thr Ile  
 385 390 395 400  
 Asn Ile Asn Gly Leu Ile Ser Lys Glu Thr Val Gln Lys Ala Val Ala  
 405 410 415  
 Asp Asn Val Xaa Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu Glu Lys  
 420 425 430  
 Ala Lys Gly Glu Gly Pro Phe Thr Ala Gly Val Asn His Val Ile Pro  
 435 440 445  
 Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu Leu Lys  
 450 455 460  
 Ala Ser Asp Lys Ala Pro Trp Ser Asp Asn Gly Asp Ala Lys Asn Pro  
 465 470 475 480  
 Ala Leu Ser Pro Leu Gly Glu Asn Val Lys Thr Lys Gly Gln Tyr Phe  
 485 490 495  
 Tyr Gln Xaa Ala Leu Asp Gly Asn Val Ala Gly Lys Glu Lys Gln Ala  
 500 505 510  
 Leu Ile Asp Gln Phe Arg Ala Asn Gly Thr Gln Thr Tyr Ser Ala Thr  
 515 520 525  
 Val Asn Val Tyr Gly Asn Lys Asp Gly Lys Pro Asp Leu Asp Asn Ile  
 530 535 540  
 Val Ala Thr Lys Lys Val Thr Ile Lys Ile Asn Val Lys Glu Thr Ser  
 545 550 555 560  
 Asp Thr Ala Asn Gly Ser Leu Ser Pro Ser Asn Ser Gly Ser Gly Val  
 565 570 575  
 Thr Pro Met Asn His Asn His Ala Thr Gly Thr Thr Asp Ser Met Pro  
 580 585 590  
 Ala Asp Thr Met Thr Ser Ser Thr Asn Thr Met Ala Gly Glu Asn Met  
 595 600 605

Ala Ala Ser Ala Asn Lys Met Ser Asp Thr Met Met Ser Glu Asp Lys  
610 615 620

Ala Met  
625

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 593 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

TTCCAATCAA AAACAGGCAG ATGGTAAACT CAATATCGTG ACAACCTTTT ACCCTGTCTA 60  
 TGA rTTTACC AAGCAAGTCG CAGGAGATAC GGCTAATGTA GAACTCCTAA TCGGTGCTGG 120  
 GACAGAACCT CATGAATACG AACCATCTGC CAAGGCAGTT GCCAAAATCC AAGATGCAGA 180  
 TACCTTCGTT TATGAAAATG AAAACATGGA AACATGGGTA CCTAAATTGC TAGATACCTT 240  
 GGATAAGAAA AAAGTGAAAA CCATCAAGGC GACAGGCGAT ATGTTGCTCT TGCCAGGTGG 300  
 CGAGGAAGAA GAGGGAGACC ATGACCATGG AGAAGAAGGT CATCACCATG AGTTTGACCC 360  
 CCATGTTTGG TTATCACCAG TTCGTGCCAT tAAACTAGTA GAGCACCATC CGCGACACTT 420  
 GTCAGCAGAT TATCCTGATA AAAAAGAGAC CTTTGAGAAG AATGCAGCTG CCTATATCGA 480  
 AAAATTGCAA GCCTTGATA AGGCTTACGC AGAAGGTTTG TCTCAAGCAA AACAAAAGAG 540  
 CTTTGTGACT CAACACGCag CCTTTAACTa TCTTGCCTTG GACTATGGGA CTC 593

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 197 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Ser Asn Gln Lys Gln Ala Asp Gly Lys Leu Asn Ile Val Thr Thr Phe  
1 5 10 15  
 Tyr Pro Val Tyr Glu Phe Thr Lys Gln Val Ala Gly Asp Thr Ala Asn  
20 25 30  
 Val Glu Leu Leu Ile Gly Ala Gly Thr Glu Pro His Glu Tyr Glu Pro  
35 40 45  
 Ser Ala Lys Ala Val Ala Lys Ile Gln Asp Ala Asp Thr Phe Val Tyr  
50 55 60  
 Glu Asn Glu Asn Met Glu Thr Trp Val Pro Lys Leu Leu Asp Thr Leu

65		70		75		80									
Asp	Lys	Lys	Lys	Val	Lys	Thr	Ile	Lys	Ala	Thr	Gly	Asp	Met	Leu	Leu
				85					90					95	
Leu	Pro	Gly	Gly	Glu	Glu	Glu	Glu	Gly	Asp	His	Asp	His	Gly	Glu	Glu
			100					105					110		
Gly	His	His	His	Glu	Phe	Asp	Pro	His	Val	Trp	Leu	Ser	Pro	Val	Arg
			115				120					125			
Ala	Ile	Lys	Leu	Val	Glu	His	His	Pro	Arg	His	Leu	Ser	Ala	Asp	Tyr
	130					135					140				
Pro	Asp	Lys	Lys	Glu	Thr	Phe	Glu	Lys	Asn	Ala	Ala	Ala	Tyr	Ile	Glu
145					150				155						160
Lys	Leu	Gln	Ala	Leu	Asp	Lys	Ala	Tyr	Ala	Glu	Gly	Leu	Ser	Gln	Ala
				165					170					175	
Lys	Gln	Lys	Ser	Phe	Val	Thr	Gln	His	Ala	Ala	Phe	Asn	Tyr	Leu	Ala
			180					185					190		
Leu	Asp	Tyr	Gly	Thr											
			195												

## (2) INFORMATION FOR SEQ ID NO: 109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

TATCACAGGA	TCGAACGGTA	AGACAACCAC	AACGACTATG	ATTGGGGAAG	TTTTGACTGC	60
TGCTGGCCAA	CATGGTCTTT	TATCAGGGAA	TATCGGCTAT	CCAGCTAGTC	AGGTTGCTCA	120
AATAGCATCA	GATAAGGACA	CGCTTGTTAT	GGAACTTTCT	TCTTTCCAAC	TCATGGGTGT	180
TCAAGAATTC	CATCCAGAGA	TTGCGGTAT	TACCAACCTC	ATGCCAACTC	ATATCGACTA	240
CCATGGGTCA	TTTTCGGAAT	ATGTAGCAGC	CAAGTGGAAT	ATCCAGAACA	AGATGACAGC	300
AGCTGATTTT	CTTGCTTTGA	ACTTTAATCA	AGACTTGGCA	AAAGACTTGA	CTTCCAAGAC	360
AGAAGCCACT	GTTGTACCAT	TTTCAACACT	TGAAAAGGTT	GATGGAGCTT	ATCTGGAAGA	420
TGGTCAACTC	TACTTCCGTG	GTGAAGTAGT	CATGGCAGCG	AATGAAATCG	GTGTTCCAGG	480
TAGCCACAAT	GTGGAAAATG	CCCTTGCGAC	TATTGCTGTA	GCCAAGCTTC	GTGATGTGGA	540
CAATCAAACC	ATCAAGGAAA	CTCTTTCAGC	CTTCGGTGGT	GTCAAACACC	GTCTCCAGTT	600
TGTGGATGAC	ATCAAGGGTG	TTAAATTCTA	TAACGACAGT	AAATCAACTA	ATATCTTGGC	660
TACTCAAAAA	GCCTTGTCAG	GATTTGACAA	CAGCAAGGTC	GTCTTGATTG	CAGGTGGTTT	720
GGACCGTGGC	AATGAGTTTG	ACGAATTGGT	GCCAGACATT	ACTGGACTCA	AGAAGATGGT	780

CATCCTGGGT CAATCTGCAG AACGTGTCAA ACGGGCAGCA GACAAGGCTG GTGTCGCTTA 840  
 TGTGGAGGCG ACAGATATTG CAGATGCGAC CCGCAAGGCC TATGAGCTTG CGACTCAAGG 900  
 AGATGTGGTT CTTCTTAGTC CTGCCAATGC TAGCTGGGAT ATGTATGCTA ACTTTGAAGT 960  
 ACGTGGCGAC CTCTTTATCG ACACAGTAGC GGAGTTAAAA GAA 1003

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Gly Ile Thr Gly Ser Asn Gly Lys Thr Thr Thr Thr Thr Met Ile Gly  
 1 5 10 15  
 Glu Val Leu Thr Ala Ala Gly Gln His Gly Leu Leu Ser Gly Asn Ile  
 20 25 30  
 Gly Tyr Pro Ala Ser Gln Val Ala Gln Ile Ala Ser Asp Lys Asp Thr  
 35 40 45  
 Leu Val Met Glu Leu Ser Ser Phe Gln Leu Met Gly Val Gln Glu Phe  
 50 55 60  
 His Pro Glu Ile Ala Val Ile Thr Asn Leu Met Pro Thr His Ile Asp  
 65 70 75 80  
 Tyr His Gly Ser Phe Ser Glu Tyr Val Ala Ala Lys Trp Asn Ile Gln  
 85 90 95  
 Asn Lys Met Thr Ala Ala Asp Phe Leu Val Leu Asn Phe Asn Gln Asp  
 100 105 110  
 Leu Ala Lys Asp Leu Thr Ser Lys Thr Glu Ala Thr Val Val Pro Phe  
 115 120 125  
 Ser Thr Leu Glu Lys Val Asp Gly Ala Tyr Leu Glu Asp Gly Gln Leu  
 130 135 140  
 Tyr Phe Arg Gly Glu Val Val Met Ala Ala Asn Glu Ile Gly Val Pro  
 145 150 155 160  
 Gly Ser His Asn Val Glu Asn Ala Leu Ala Thr Ile Ala Val Ala Lys  
 165 170 175  
 Leu Arg Asp Val Asp Asn Gln Thr Ile Lys Glu Thr Leu Ser Ala Phe  
 180 185 190  
 Gly Gly Val Lys His Arg Leu Gln Phe Val Asp Asp Ile Lys Gly Val  
 195 200 205  
 Lys Phe Tyr Asn Asp Ser Lys Ser Thr Asn Ile Leu Ala Thr Gln Lys  
 210 215 220  
 Ala Leu Ser Gly Phe Asp Asn Ser Lys Val Val Leu Ile Ala Gly Gly

225		230		235		240
Leu Asp Arg Gly	Asn Glu Phe Asp Glu	Leu Val Pro Asp Ile Thr Gly				
	245	250			255	
Leu Lys Lys Met	Val Ile Leu Gly Gln Ser Ala Glu Arg Val Lys Arg					
	260	265			270	
Ala Ala Asp Lys	Ala Gly Val Ala Tyr Val Glu Ala Thr Asp Ile Ala					
	275	280			285	
Asp Ala Thr Arg	Lys Ala Tyr Glu Leu Ala Thr Gln Gly Asp Val Val					
	290	295		300		
Leu Leu Ser Pro	Ala Asn Ala Ser Trp Asp Met Tyr Ala Asn Phe Glu					
	305	310		315		320
Val Arg Gly Asp	Leu Phe Ile Asp Thr Val Ala Glu Leu Lys Glu					
	325	330			335	

## (2) INFORMATION FOR SEQ ID NO: 111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AAGTTCATCG AAGATGGTTG GGAAGTCCAC TATATCGGGG ACAAGTGTGG TATCGAACAC	60
CAAGAAATCC TTAAGTCAGG TTTGGATGTC ACCTTCCATT CTATTGCGAC TGGAAAATTG	120
CGTCGCTATT TCTCTTGGCA AAATATGCTG GACGTCTTCA AAGTTGGTTG GGGAATTGTC	180
CAATCGCTCT TTATCATGTT GCGACTGCGT CCACAGACCC TTTTTTCAAA GGGGGGCTTT	240
GTCTCAGTAC CGCCTGTTAT CGCTGCGCGT GTGTCAGGAG TGCCTGTCTT TATTCACGAA	300
TCTGACCTGT CTATGGGCTT GGCCAATAAA ATCGCCTATA AATTTGCGAC TAAGATGTAT	360
TCAACCTTTG AACAAGCTTC GAGTTTGGCT AAGGTTGAGC ATGTGGGAGC GG	412

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ser Ser Ser Lys Met Val Gly Lys Ser Thr Ile Ser Gly Thr Ser Val	
1	5 10 15
Val Ser Asn Thr Lys Lys Ser Leu Ser Gln Val Trp Met Ser Pro Ser	
	20 25 30

Ile Leu Leu Arg Leu Glu Asn Cys Val Ala Ile Ser Leu Gly Lys Ile  
 35 40 45  
 Cys Trp Thr Ser Ser Lys Leu Val Gly Glu Leu Ser Asn Arg Ser Leu  
 50 55 60  
 Ser Cys Cys Asp Cys Val His Arg Pro Phe Phe Gln Arg Gly Ala Leu  
 65 70 75 80  
 Ser Gln Tyr Arg Leu Leu Ser Leu Arg Val Cys Gln Glu Cys Leu Ser  
 85 90 95  
 Leu Phe Thr Asn Leu Thr Cys Leu Trp Ala Trp Pro Ile Lys Ser Pro  
 100 105 110  
 Ile Asn Leu Arg Leu Arg Cys Ile Gln Pro Leu Asn Lys Leu Arg Val  
 115 120 125  
 Trp Leu Arg Leu Ser Met Trp Glu Arg  
 130 135

## (2) INFORMATION FOR SEQ ID NO: 113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ATCGCTAGCT AGTGAAATGC AAGAAAGTAC ACGTAAATTC AAGGTTACTG CTGACCTAAC 60  
 AGATGCCCGGT GTTGAACGA TTGAAGTTCC TTTGAGCATT GAAGATTTAC CCAATGGGCT 120  
 GACCGCTGTG GCGACTCCGC AAAAAATTAC AGTCAAGATT GGTAAGAAGG CTCAGAAGGA 180  
 TAAGGTAAAG ATTGTACCAG AGATTGACCC TAGTCAAATT GATAGTCGGG TACAAATTGA 240  
 AAATGTCATG GTGTCAGATA AAGAAGTGTC TATTACGAGT GACCAAGAGA CATTGGATAG 300  
 AATTGATAAG ATTATCGCTG TTTTGCCAAC TAGCGAACGT ATAACAGGTA ATTACAGTGG 360  
 TTCAGTACCT TTGCAGGCAA TCGACCGCAA TGGTGTGTGTC TTACCGGCAG TTATCACTCC 420  
 GTTTGATACA ATAATGAAGG TGA CTACAAA ACCAGTAGCA CCAAGTTCAA GCACATCAAA 480  
 TTCAAGTACA AGCAGTTCAT CGGAGACATC TTCGTCAACG AAAGCAACTA GTTCAAAAAC 540  
 GAAT 544


## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:



Ser Leu Ala Ser Glu Met Gln Glu Ser Thr Arg Lys Phe Lys Val Thr  
 1 5 10 15  
 Ala Asp Leu Thr Asp Ala Gly Val Gly Thr Ile Glu Val Pro Leu Ser  
 20 25 30  
 Ile Glu Asp Leu Pro Asn Gly Leu Thr Ala Val Ala Thr Pro Gln Lys  
 35 40 45  
 Ile Thr Val Lys Ile Gly Lys Lys Ala Gln Lys Asp Lys Val Lys Ile  
 50 55 60  
 Val Pro Glu Ile Asp Pro Ser Gln Ile Asp Ser Arg Val Gln Ile Glu  
 65 70 75 80  
 Asn Val Met Val Ser Asp Lys Glu Val Ser Ile Thr Ser Asp Gln Glu  
 85 90 95  
 Thr Leu Asp Arg Ile Asp Lys Ile Ile Ala Val Leu Pro Thr Ser Glu  
 100 105 110  
 Arg Ile Thr Gly Asn Tyr Ser Gly Ser Val Pro Leu Gln Ala Ile Asp  
 115 120 125  
 Arg Asn Gly Val Val Leu Pro Ala Val Ile Thr Pro Phe Asp Thr Ile  
 130 135 140  
 Met Lys Val Thr Thr Lys Pro Val Ala Pro Ser Ser Ser Thr Ser Asn  
 145 150 155 160  
 Ser Ser Thr Ser Ser Ser Ser Glu Thr Ser Ser Ser Thr Lys Ala Thr  
 165 170 175  
 Ser Ser Lys Thr Asn  
 180

## (2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1267 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GCACCAGATG GGGCACAAGG TTCAGGGATC AGATGTTGAA AAGTACTACT TTACCCAACG 60  
 CGGTCTTGAG CAGGCAGGAA TTACCATTTCT TCCTTTTGAT GAAAAAATC TAGACGGTGA 120  
 TATGGAAATT ATCGCTGGAA ATGCCTTTCG TCCAGATAAC AACGTCGAAA TTGCCTATGC 180  
 GGACCAAAAT GGTATCAGCT ACAAACGTTA CCATGAGTTT CTAGGTAGCT TTATGCGTGA 240  
 CTTTGTTAGC ATGGGAGTAG CAGGAGCACA TGGAAAAACT TCAACGACAG GTATGTTGTC 300  
 TCATGTCTTG TCTCACATTA CAGATACCAG CTTCTTGATT GGAGATGGGA CAGGTCGTGG 360  
 TTCGGCCAAT GCCAAATATT TTGTCTTTGA ATCTGACGAA TATGAGCGTC ACTTCATGCC 420

TTACCACCCA GAATACTCTA TTATCACCAA CATTGACTTT GACCATCCAG ATTATTTTCAC 480  
 AAGTCTCGAG GATGTTTTTA ATGCCTTTAA CGACTATGCC AAACAAATCA CCAAGGGTCT 540  
 TTTTGTCTAT GGTGAAGATG CTGAATTGCG TAAGATTACG TCTGATGCAC CAATTTATTA 600  
 TTATGGTTTT GAAGCTGAAG GCAATGACTT TGTAGCTAGT GATCTTCTTC GTTCAATAAC 660  
 TGGTTCAACC TTCACCGTTC ATTTCCGTGG ACAAACCTTG GGGCAATTCC ACATTCCAAC 720  
 CTTTGGTCGT CACAATATCA TGAATGCGAC AGCCGTTATT GGTCTTCTTT ACACAGCAGG 780  
 ATTTGATTTG AACTTGGTGC GTGAGCACTT GAAAACATTT GCCGGTGTTA AACGTCGTTT 840  
 CACTGAGAAA ATTGTCAATG ATACAGTGAT TATCGATGAC TTTGCCCACC ATCCAACAGA 900  
 AATTATTGCG ACCTTGGATG CGGCTCGTCA GAAATACCCA AGCAAGGAAA TTGTAGCAGT 960  
 CTTTCAACCG CATACTTTA CAAGAACCAT TGCCTTGTTG GACGACTTTG CCCATGCTTT 1020  
 AAACCAAGCA GATGCTGTTT ATCTAGCGCA AATTTATGGC TCGGCTCGTG AAGTAGATCA 1080  
 TGGTGACGTT AAGGTAGAAG ACCTAGCCAA CAAATCAAC AAAAAACACC AAGTGATTAC 1140  
 TGTTGAAAAT GTTTCTCCAC TCCTAGACCA TGACAATGCT GTTTACGTCT TTATGGGAGC 1200  
 AGGAGACATC CAAACCTATG AATACTCATT TGAGCGTCTC TTGTCTAACT TGACAAGCAA 1260  
 TGTTCOA 1267

(2) INFORMATION FOR SEQ ID NO:116:


- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 422 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

His	Gln	Met	Gly	His	Lys	Val	Gln	Gly	Ser	Asp	Val	Glu	Lys	Tyr	Tyr
1				5					10					15	
Phe	Thr	Gln	Arg	Gly	Leu	Glu	Gln	Ala	Gly	Ile	Thr	Ile	Leu	Pro	Phe
			20					25					30		
Asp	Glu	Lys	Asn	Leu	Asp	Gly	Asp	Met	Glu	Ile	Ile	Ala	Gly	Asn	Ala
		35				40						45			
Phe	Arg	Pro	Asp	Asn	Asn	Val	Glu	Ile	Ala	Tyr	Ala	Asp	Gln	Asn	Gly
	50					55					60				
Ile	Ser	Tyr	Lys	Arg	Tyr	His	Glu	Phe	Leu	Gly	Ser	Phe	Met	Arg	Asp
65				70						75				80	
Phe	Val	Ser	Met	Gly	Val	Ala	Gly	Ala	His	Gly	Lys	Thr	Ser	Thr	Thr
				85					90					95	
Gly	Met	Leu	Ser	His	Val	Leu	Ser	His	Ile	Thr	Asp	Thr	Ser	Phe	Leu
			100					105					110		





Ile Gly Asp Gly Thr Gly Arg Gly Ser Ala Asn Ala Lys Tyr Phe Val  
 115 120 125  
 Phe Glu Ser Asp Glu Tyr Glu Arg His Phe Met Pro Tyr His Pro Glu  
 130 135 140  
 Tyr Ser Ile Ile Thr Asn Ile Asp Phe Asp His Pro Asp Tyr Phe Thr  
 145 150 155 160  
 Ser Leu Glu Asp Val Phe Asn Ala Phe Asn Asp Tyr Ala Lys Gln Ile  
 165 170 175  
 Thr Lys Gly Leu Phe Val Tyr Gly Glu Asp Ala Glu Leu Arg Lys Ile  
 180 185 190  
 Thr Ser Asp Ala Pro Ile Tyr Tyr Tyr Gly Phe Glu Ala Glu Gly Asn  
 195 200 205  
 Asp Phe Val Ala Ser Asp Leu Leu Arg Ser Ile Thr Gly Ser Thr Phe  
 210 215 220  
 Thr Val His Phe Arg Gly Gln Asn Leu Gly Gln Phe His Ile Pro Thr  
 225 230 235 240  
 Phe Gly Arg His Asn Ile Met Asn Ala Thr Ala Val Ile Gly Leu Leu  
 245 250 255  
 Tyr Thr Ala Gly Phe Asp Leu Asn Leu Val Arg Glu His Leu Lys Thr  
 260 265 270  
 Phe Ala Gly Val Lys Arg Arg Phe Thr Glu Lys Ile Val Asn Asp Thr  
 275 280 285  
 Val Ile Ile Asp Asp Phe Ala His His Pro Thr Glu Ile Ile Ala Thr  
 290 295 300  
 Leu Asp Ala Ala Arg Gln Lys Tyr Pro Ser Lys Glu Ile Val Ala Val  
 305 310 315 320  
 Phe Gln Pro His Thr Phe Thr Arg Thr Ile Ala Leu Leu Asp Asp Phe  
 325 330 335  
 Ala His Ala Leu Asn Gln Ala Asp Ala Val Tyr Leu Ala Gln Ile Tyr  
 340 345 350  
 Gly Ser Ala Arg Glu Val Asp His Gly Asp Val Lys Val Glu Asp Leu  
 355 360 365  
 Ala Asn Lys Ile Asn Lys Lys His Gln Val Ile Thr Val Glu Asn Val  
 370 375 380  
 Ser Pro Leu Leu Asp His Asp Asn Ala Val Tyr Val Phe Met Gly Ala  
 385 390 395 400  
 Gly Asp Ile Gln Thr Tyr Glu Tyr Ser Phe Glu Arg Leu Leu Ser Asn  
 405 410 415  
 Leu Thr Ser Asn Val Gln  
 420

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

TTTTAACCCA ACTGTTGGTA CTTTCCTTTT TACTGCAGGA TTGAGCTTGT TAGTTTTATT 60  
 GGTTCCTAAA AGGGAAAATG GAAAGAAACG ACTTGTTTCAT TTTCTGCTGT TGACTAGCAT 120  
 GGGAGTTCAA TTGTTGCCGG CCAGTGCTTT TGGGTTGACC AGCCAGATTT TATCTGCCTA 180  
 TAATAGTCAG CTTTCTATCG GAGTCGGGGA ACATTTACCA GAGCCTCTGA AAATCGAAGG 240  
 TTATCAATAT ATTGGTTATA TCAAAACTAA GAAACAGGAT AATACAGAGC TTTCAAGGAC 300  
 AGTTGATGGG AAATACTCTG CTCAAAGAGA TAGTCAACCA AACTCTACAA AAACATCAGA 360  
 TGTAGTTCAT TCAGCTGATT TAGAATGGAA CCAAGGACAG GGAAGGTTA GTTTACAAGG 420  
 TGAAGCATCA GGGGATGATG GACTTTTCAGA AAAATCTTCT ATAGCAGCAG ACAATCTATC 480  
 TTCTAATGAT TCATTCGCAA GTCAAGTTGA GCAGAATCCG GATCACAAAG GAGAATCTGT 540  
 AGTTCGACCA ACAGTGCCAG AACAAGGAAA TCCTGTGTCT GCTACAACGG TGCAGAGTGC 600  
 GGAAGAGGAA GTATTGGCGA CGACAAATGA TCGACCAGAG TATAAACTTC CATTGGAAAC 660  
 CAAAGGCACG CAAGAACCCG GTCATGAGGG TGAAGCCGCA GTCCGTGAAG ACTTACCAGT 720  
 CTACACTAAG CCACTAGAAA CCAAAGGTAC ACAAGGACCC GGACATGAAG GTGAAGCTGC 780  
 AGTTCGCGAG GAAGAACCAG CTTACACAGA ACCGTTAGCA ACGAAAGGCA CGCAAGAGCC 840  
 AGGTCATGAG GGCAAAGCTA CAGTCCGCGA AGAGACTCTA GAGTACACGG AACCGGTAGC 900  
 GACAAAAGGC ACACAAGAAC CCGAACATGA GGGCGAaCGG sCAGTAGAAG AAGAACTTCC 960  
 GGCTTTTAGAG GTCACTACAC GAAATAGAAC GGAAATCCAG AATATTCCTT ATACAACAGA 1020  
 AGAAATTCAG GATCCAACAC TTCTGAAAAA TCGTCGTAAG ATTGAACGAC AAGGGCAAGC 1080  
 AGGGACACGT ACAATTCAAT ATGAAGACTA CATCGTAAAT GGTAAATGTCG TAGAACTAA 1140  
 AGAAGTGTC ACGAACTGAAG TAGCTCCGGT CAACGAAGTC GTTAAAGTAG GAACACTTGT 1200  
 GAAAGTTAAA CCTACAGTAG AAATTACAAA CTTAACAAAA GTTGAGAACA AAAAATCTAT 1260  
 AACTGTAAGT TATAACTTAA TAGACACTAC CTCAGCATAT GTTTCTGCAA AAACGCAAGT 1320  
 TTTCCATGGA GACAAGCTAG TTAAAGAGGT GGATATAGAA AATCCTGCCA AAGAGCAAGT 1380  
 AATATCAGGT TTAGATTACT ACACACCGTA TACAGTTAAA ACACACCTAA CTTATAATTT 1440  
 GGGTGAAAAT AATGAGGAAA ATACTGAAAC ATCAACTCAA GATTTCCAAT TAGAGTATAA 1500  
 GAAAAATAGAG ATTAAAGATA TTGATTTCAGT AGAATTATAC GGTAAAGAAA ATGATCGTTA 1560  
 TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT 1620  
 GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA 1680



TGGAACGTAT	AAAGTGACGG	TAGCCGTTGA	TCAACTTGTC	GAAGAAGGTA	CAGACGGTTA	1740
CAAAGATGAT	TACACATTTA	CTGTAGCTAA	ATCTAAAGCA	GAGCAACCAG	GAGTTTACAC	1800
ATCCTTTAAA	CAGCTGGTAA	CAGCCATGCA	AAGCAATCTG	TCTGGTGTCT	ATACATTGGC	1860
TTCAGATATG	ACCGCAGATG	AGGTGAGCTT	AGGCGATAAG	CAGACAAGTT	ATCTCACAGG	1920
TGCATTTACA	GGGAGCTTGA	TCGGTTCTGA	TGGAACAAAA	TCGTATGCCA	TTTATGATTT	1980
GAAGAAACCA	TTATTTGATA	CATTAAATGG	TGCTACAGTT	AGAGATTTGG	ATATTAAAAAC	2040
TGTTTCTGCT	GATAGTAAAG	AAAATGTCGC	AGCGCTGGCG	AAGGCAGCGA	ATAGCGCGAA	2100
TATTAATAAT	GTTGCAGTAG	AAGGAAAAAT	CTCAGGTGCG	AAATCTGTTG	CGGGATTAGT	2160
AGCGAGCGCA	ACAAATACAG	TGATAGAAAA	CAGCTCGTTT	ACAGGGAAAC	TTATCGCAAA	2220
TCACCAGGAC	AGTAATAAAA	ATGATACTGG	AGGAATAGTA	GGTAATATAA	CAGGAAATAG	2280
TTCGAGAGTT	AATAAAGTTA	GGGTAGATGC	CTTAATCTCT	ACTAATGCAC	GCAATAATAA	2340
CCAAACAGCT	GGAGGGATAG	TAGGTAGATT	AGAAAATGGT	GCATTGATAT	CTAATTCGGT	2400
TGCTACTGGA	GAAATACGAA	ATGGTCAAGG	ATATTCTAGA	GTCGGAGGAA	TAGTAGGATC	2460
TACGTGGCAA	AACGGTCGAG	TAAATAATGT	TGTGAGTAAC	GTAGATGTTG	GAGATGGTTA	2520
TGTTATCACC	GGTGATCAAT	ACGCAGCAGC	AGATGTGAAA	AATGCAAGTA	CATCAGTTGA	2580
TAATAGAAAA	GCAGACAGAT	TCGCTACAAA	ATTATCAAAA	GACCAAATAG	ACGCGAAAAGT	2640
TGCTGATTAT	GGAATCACAG	TAACTCTTGA	TGATACTGGG	CAAGATTTAA	AACGTAATCT	2700
AAGAGAAGTT	GATTATACAA	GACTAAATAA	AGCAGAAGCT	GAAAGAAAAG	TAGCTTATAG	2760
CAACATAGAA	AAACTGATGC	CATTCTACAA	TAAAGACCTA	GTAGTTCACT	ATGGTAACAA	2820
AGTAGCGACA	ACAGATAAAC	TTTACACTAC	AGAATTGTTA	GATGTTGTGC	CGATGAAAGA	2880
TGATGAAGTA	GTAACGGATA	TTAATAATAA	GAAAAATTCA	ATAAATAAAG	TTATGTTACA	2940
TTTCAAAGAT	AATACAGTAG	AATACCTAGA	TGTAACATTC	AAAGAAAAC	TCATAAACAG	3000
TCAAGTAATC	GAATACAATG	TTACAGGAAA	AGAATATATA	TTCACACCAG	AAGCATTTGT	3060
TTCAGACTAT	ACAGCGATAA	CGAATAACGT	ACTAAGCGAC	TTGCAAAATG	TAACACTTAA	3120
C						3121

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu  
 1 5 10 15  
 Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val  
 20 25 30  
 His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser  
 35 40 45  
 Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu  
 50 55 60  
 Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly  
 65 70 75 80  
 Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu  
 85 90 95  
 Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln  
 100 105 110  
 Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu  
 115 120 125  
 Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly  
 130 135 140  
 Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser  
 145 150 155 160  
 Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys  
 165 170 175  
 Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val  
 180 185 190  
 Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr  
 195 200 205  
 Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln  
 210 215 220  
 Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val  
 225 230 235 240  
 Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu  
 245 250 255  
 Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu  
 260 265 270  
 Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val  
 275 280 285  
 Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr  
 290 295 300  
 Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro  
 305 310 315 320  
 Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro  
 325 330 335  
 Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg

				340				345				350			
Lys	Ile	Glu	Arg	Gln	Gly	Gln	Ala	Gly	Thr	Arg	Thr	Ile	Gln	Tyr	Glu
		355					360					365			
Asp	Tyr	Ile	Val	Asn	Gly	Asn	Val	Val	Glu	Thr	Lys	Glu	Val	Ser	Arg
		370					375					380			
Thr	Glu	Val	Ala	Pro	Val	Asn	Glu	Val	Val	Lys	Val	Gly	Thr	Leu	Val
		385					390					395			
Lys	Val	Lys	Pro	Thr	Val	Glu	Ile	Thr	Asn	Leu	Thr	Lys	Val	Glu	Asn
							405					410			415
Lys	Lys	Ser	Ile	Thr	Val	Ser	Tyr	Asn	Leu	Ile	Asp	Thr	Thr	Ser	Ala
							420					425			430
Tyr	Val	Ser	Ala	Lys	Thr	Gln	Val	Phe	His	Gly	Asp	Lys	Leu	Val	Lys
							435					440			
Glu	Val	Asp	Ile	Glu	Asn	Pro	Ala	Lys	Glu	Gln	Val	Ile	Ser	Gly	Leu
							445					450			
Asp	Tyr	Tyr	Thr	Pro	Tyr	Thr	Val	Lys	Thr	His	Leu	Thr	Tyr	Asn	Leu
							455					460			
Gly	Glu	Asn	Asn	Glu	Glu	Asn	Thr	Glu	Thr	Ser	Thr	Gln	Asp	Phe	Gln
							465					470			
Leu	Glu	Tyr	Lys	Lys	Ile	Glu	Ile	Lys	Asp	Ile	Asp	Ser	Val	Glu	Leu
							475					480			
Tyr	Gly	Lys	Glu	Asn	Asp	Arg	Tyr	Arg	Arg	Tyr	Leu	Ser	Leu	Ser	Glu
							485					490			
Ala	Pro	Thr	Asp	Thr	Ala	Lys	Tyr	Phe	Val	Lys	Val	Lys	Ser	Asp	Arg
							495					500			
Phe	Lys	Glu	Met	Tyr	Leu	Pro	Val	Lys	Ser	Ile	Thr	Glu	Asn	Thr	Asp
							505					510			
Gly	Thr	Tyr	Lys	Val	Thr	Val	Ala	Val	Asp	Gln	Leu	Val	Glu	Glu	Gly
							515					520			
Thr	Asp	Gly	Tyr	Lys	Asp	Asp	Tyr	Thr	Phe	Thr	Val	Ala	Lys	Ser	Lys
							525					530			
Ala	Glu	Gln	Pro	Gly	Val	Tyr	Thr	Ser	Phe	Lys	Gln	Leu	Val	Thr	Ala
							535					540			
Met	Gln	Ser	Asn	Leu	Ser	Gly	Val	Tyr	Thr	Leu	Ala	Ser	Asp	Met	Thr
							545					550			
Ala	Asp	Glu	Val	Ser	Leu	Gly	Asp	Lys	Gln	Thr	Ser	Tyr	Leu	Thr	Gly
							555					560			
Ala	Phe	Thr	Gly	Ser	Leu	Ile	Gly	Ser	Asp	Gly	Thr	Lys	Ser	Tyr	Ala
							565					570			
Ile	Tyr	Asp	Leu	Lys	Lys	Pro	Leu	Phe	Asp	Thr	Leu	Asn	Gly	Ala	Thr
							575					580			
Val	Arg	Asp	Leu	Asp	Ile	Lys	Thr	Val	Ser	Ala	Asp	Ser	Lys	Glu	Asn
							585					590			

Val Ala Ala Leu Ala Lys Ala Ala Asn Ser Ala Asn Ile Asn Asn Val  
 690 695 700  
 Ala Val Glu Gly Lys Ile Ser Gly Ala Lys Ser Val Ala Gly Leu Val  
 705 710 715 720  
 Ala Ser Ala Thr Asn Thr Val Ile Glu Asn Ser Ser Phe Thr Gly Lys  
 725 730 735  
 Leu Ile Ala Asn His Gln Asp Ser Asn Lys Asn Asp Thr Gly Gly Ile  
 740 745 750  
 Val Gly Asn Ile Thr Gly Asn Ser Ser Arg Val Asn Lys Val Arg Val  
 755 760 765  
 Asp Ala Leu Ile Ser Thr Asn Ala Arg Asn Asn Asn Gln Thr Ala Gly  
 770 775 780  
 Gly Ile Val Gly Arg Leu Glu Asn Gly Ala Leu Ile Ser Asn Ser Val  
 785 790 795 800  
 Ala Thr Gly Glu Ile Arg Asn Gly Gln Gly Tyr Ser Arg Val Gly Gly  
 805 810 815  
 Ile Val Gly Ser Thr Trp Gln Asn Gly Arg Val Asn Asn Val Val Ser  
 820 825 830  
 Asn Val Asp Val Gly Asp Gly Tyr Val Ile Thr Gly Asp Gln Tyr Ala  
 835 840 845  
 Ala Ala Asp Val Lys Asn Ala Ser Thr Ser Val Asp Asn Arg Lys Ala  
 850 855 860  
 Asp Arg Phe Ala Thr Lys Leu Ser Lys Asp Gln Ile Asp Ala Lys Val  
 865 870 875 880  
 Ala Asp Tyr Gly Ile Thr Val Thr Leu Asp Asp Thr Gly Gln Asp Leu  
 885 890 895  
 Lys Arg Asn Leu Arg Glu Val Asp Tyr Thr Arg Leu Asn Lys Ala Glu  
 900 905 910  
 Ala Glu Arg Lys Val Ala Tyr Ser Asn Ile Glu Lys Leu Met Pro Phe  
 915 920 925  
 Tyr Asn Lys Asp Leu Val Val His Tyr Gly Asn Lys Val Ala Thr Thr  
 930 935 940  
 Asp Lys Leu Tyr Thr Thr Glu Leu Leu Asp Val Val Pro Met Lys Asp  
 945 950 955 960  
 Asp Glu Val Val Thr Asp Ile Asn Asn Lys Lys Asn Ser Ile Asn Lys  
 965 970 975  
 Val Met Leu His Phe Lys Asp Asn Thr Val Glu Tyr Leu Asp Val Thr  
 980 985 990  
 Phe Lys Glu Asn Phe Ile Asn Ser Gln Val Ile Glu Tyr Asn Val Thr  
 995 1000 1005  
 Gly Lys Glu Tyr Ile Phe Thr Pro Glu Ala Phe Val Ser Asp Tyr Thr  
 1010 1015 1020

Ala Ile Thr Asn Asn Val Leu Ser Asp Leu Gln Asn Val Thr Leu Asn  
 1025 1030 1035 1040

## (2) INFORMATION FOR SEQ ID NO: 119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TTTTAACCCA ACTGTTGGTA CTTTCCTTTT TACTGCAGGA TTGAGCTTGT TAGTTTTATT 60  
 GGTTCCTAAA AGGGAAAATG GAAAGAAACG ACTTGTTTCAT TTTCTGCTGT TGACTAGCAT 120  
 GGGAGTTCAA TTGTTGCCGG CCAGTGCTTT TGGGTTGACC AGCCAGATTT TATCTGCCTA 180  
 TAATAGTCAG CTTTCCTATCG GAGTCGGGGA ACATTTACCA GAGCCTCTGA AAATCGAAGG 240  
 TTATCAATAT ATTGGTTATA TCAAACTAA GAAACAGGAT AATACAGAGC TTTCAAGGAC 300  
 AGTTGATGGG AAATACTCTG CTCAAAGAGA TAGTCAACCA AACTCTACAA AAACATCAGA 360  
 TGTAGTTCAT TCAGCTGATT TAGAATGGAA CCAAGGACAG GGGAAGGTTA GTTTACAAGG 420  
 TGAAGCATCA GGGGATGATG GACTTTTCAGA AAAATCTTCT ATAGCAGCAG ACAATCTATC 480  
 TTCTAATGAT TCATTCGCAA GTCAAGTTGA GCAGAATCCG GATCACAAAG GAGAATCTGT 540  
 AGTTCGACCA ACAGTGCCAG AACAAGGAAA TCCTGTGTCT GCTACAACGG TGCAGAGTGC 600  
 GGAAGAGGAA GTATTGGCGA CGACAAATGA TCGACCAGAG TATAAACTTC CATTTGAAAC 660  
 CAAAGGCACG CAAGAACCCG GTCATGAGGG TGAAGCCGCA GTCCGTGAAG ACTTACCAGT 720  
 CTACACTAAG CCAC TAGAAA CCAAAGGTAC ACAAGGACCC GGACATGAAG GTGAAGCTGC 780  
 AGTTCGCGAG GAAGAACCAG CTTACACAGA ACCGTTAGCA ACGAAAGGCA CGCAAGAGCC 840  
 AGGTCATGAG GGCAAAGCTA CAGTCCGCGA AGAGACTCTA GAGTACACGG AACC GG TAGC 900  
 GACAAAAGGC ACACAAGAAC CCGAACATGA GGGCGAaCGG sCAGTAGAAG AAGAAC'TTCC 960  
 GGCTTTTAGAG GTCACTACAC GAAATAGAAC GGAAATCCAG AATATTCCTT ATACAACAGA 1020  
 AGAAATTCAG GATCCAACAC TTCTGAAAAA TCGTCGTAAG ATTGAACGAC AAGGGCAAGC 1080  
 AGGGACACGT ACAATTCAAT ATGAAGACTA CATCGTAAAT GGTAATGTCG TAGAAACTAA 1140  
 AGAAGTGTCA CGAACTGAAG TAGCTCCGGT CAACGAAGTC GTTAAAGTAG GAACACTTGT 1200  
 GAAAGTTAAA CCTACAGTAG AAATTACAAA CTTAACAAAA GTTGAGAACA AAAAATCTAT 1260  
 AACTGTAAGT TATAACTTAA TAGACACTAC CTCAGCATAT GTTTC'TGCAA AAACGCAAGT 1320  
 TTTCCATGGA GACAAGCTAG TTAAAGAGGT GGATATAGAA AATCCTGCCA AAGAGCAAGT 1380  
 AATATCAGGT TTAGATTACT ACACACCGTA TACAGTTAAA ACACACCTAA CTTATAATTT 1440  
 GGGTGAAAAT AATGAGGAAA ATACTGAAAC ATCAACTCAA GATTTCCAAT TAGAGTATAA 1500

GAAAATAGAG ATTAAAGATA TTGATTTCAGT AGAATTATAC GGTAAAGAAA ATGATCGTTA 1560  
TCGTAGA 1567


## (2) INFORMATION FOR SEQ ID NO:120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:



Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu  
 1 5 10 15  
 Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val  
 20 25 30  
 His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser  
 35 40 45  
 Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu  
 50 55 60  
 Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly  
 65 70 75 80  
 Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu  
 85 90 95  
 Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln  
 100 105 110  
 Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu  
 115 120 125  
 Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly  
 130 135 140  
 Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser  
 145 150 155 160  
 Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys  
 165 170 175  
 Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val  
 180 185 190  
 Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr  
 195 200 205  
 Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln  
 210 215 220  
 Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val  
 225 230 235 240  
 Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu



(2) INFORMATION FOR SEQ ID NO: 121:

(A) LENGTH: 1561 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:



TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT	60
GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA	120
TGGAACGTAT AAAGTGACGG TAGCCGTTGA TCAACTTGTC GAAGAAGGTA CAGACGGTTA	180
CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC	240
ATCCTTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC	300
TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG	360
TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT	420
GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAAC	480
TGTTTCTGCT GATAGTAAAG AAAATGTCGC AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA	540
TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT	600
AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA	660
TCACCAGGAC AGTAATAAAA ATGATAC TGG AGGAATAGTA GGTAATATAA CAGGAAATAG	720
TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA	780
CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT	840
TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC	900
TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA	960
TGTTATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA	1020
TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT	1080
TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT	1140
AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG	1200
CAACATAGAA AAACTGATGC CATTCTACAA TAAAGACCTA GTAGTTCACT ATGGTAACAA	1260
AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTTA GATGTTGTGC CGATGAAAGA	1320
TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA	1380
TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TACATAACAG	1440
TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT	1500
TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA	1560
C	1561

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Arg Arg Tyr Leu Ser Leu Ser Glu Ala Pro Thr Asp Thr Ala Lys Tyr  
 1 5 10 15  
 Phe Val Lys Val Lys Ser Asp Arg Phe Lys Glu Met Tyr Leu Pro Val  
 20 25 30  
 Lys Ser Ile Thr Glu Asn Thr Asp Gly Thr Tyr Lys Val Thr Val Ala  
 35 40 45  
 Val Asp Gln Leu Val Glu Glu Gly Thr Asp Gly Tyr Lys Asp Asp Tyr  
 50 55 60  
 Thr Phe Thr Val Ala Lys Ser Lys Ala Glu Gln Pro Gly Val Tyr Thr  
 65 70 75 80  
 Ser Phe Lys Gln Leu Val Thr Ala Met Gln Ser Asn Leu Ser Gly Val  
 85 90 95  
 Tyr Thr Leu Ala Ser Asp Met Thr Ala Asp Glu Val Ser Leu Gly Asp  
 100 105 110  
 Lys Gln Thr Ser Tyr Leu Thr Gly Ala Phe Thr Gly Ser Leu Ile Gly  
 115 120 125  
 Ser Asp Gly Thr Lys Ser Tyr Ala Ile Tyr Asp Leu Lys Lys Pro Leu  
 130 135 140  
 Phe Asp Thr Leu Asn Gly Ala Thr Val Arg Asp Leu Asp Ile Lys Thr  
 145 150 155 160  
 Val Ser Ala Asp Ser Lys Glu Asn Val Ala Ala Leu Ala Lys Ala Ala  
 165 170 175  
 Asn Ser Ala Asn Ile Asn Asn Val Ala Val Glu Gly Lys Ile Ser Gly  
 180 185 190  
 Ala Lys Ser Val Ala Gly Leu Val Ala Ser Ala Thr Asn Thr Val Ile  
 195 200 205  
 Glu Asn Ser Ser Phe Thr Gly Lys Leu Ile Ala Asn His Gln Asp Ser  
 210 215 220  
 Asn Lys Asn Asp Thr Gly Gly Ile Val Gly Asn Ile Thr Gly Asn Ser  
 225 230 235 240  
 Ser Arg Val Asn Lys Val Arg Val Asp Ala Leu Ile Ser Thr Asn Ala  
 245 250 255  
 Arg Asn Asn Asn Gln Thr Ala Gly Gly Ile Val Gly Arg Leu Glu Asn  
 260 265 270  
 Gly Ala Leu Ile Ser Asn Ser Val Ala Thr Gly Glu Ile Arg Asn Gly  
 275 280 285  
 Gln Gly Tyr Ser Arg Val Gly Gly Ile Val Gly Ser Thr Trp Gln Asn  
 290 295 300  
 Gly Arg Val Asn Asn Val Val Ser Asn Val Asp Val Gly Asp Gly Tyr  
 305 310 315 320

Val Ile Thr Gly Asp Gln Tyr Ala Ala Ala Asp Val Lys Asn Ala Ser  
 325 330 335  
 Thr Ser Val Asp Asn Arg Lys Ala Asp Arg Phe Ala Thr Lys Leu Ser  
 340 345 350  
 Lys Asp Gln Ile Asp Ala Lys Val Ala Asp Tyr Gly Ile Thr Val Thr  
 355 360 365  
 Leu Asp Asp Thr Gly Gln Asp Leu Lys Arg Asn Leu Arg Glu Val Asp  
 370 375 380  
 Tyr Thr Arg Leu Asn Lys Ala Glu Ala Glu Arg Lys Val Ala Tyr Ser  
 385 390 395 400  
 Asn Ile Glu Lys Leu Met Pro Phe Tyr Asn Lys Asp Leu Val Val His  
 405 410 415  
 Tyr Gly Asn Lys Val Ala Thr Thr Asp Lys Leu Tyr Thr Thr Glu Leu  
 420 425 430  
 Leu Asp Val Val Pro Met Lys Asp Asp Glu Val Val Thr Asp Ile Asn  
 435 440 445  
 Asn Lys Lys Asn Ser Ile Asn Lys Val Met Leu His Phe Lys Asp Asn  
 450 455 460  
 Thr Val Glu Tyr Leu Asp Val Thr Phe Lys Glu Asn Phe Ile Asn Ser  
 465 470 475 480  
 Gln Val Ile Glu Tyr Asn Val Thr Gly Lys Glu Tyr Ile Phe Thr Pro  
 485 490 495  
 Glu Ala Phe Val Ser Asp Tyr Thr Ala Ile Thr Asn Asn Val Leu Ser  
 500 505 510  
 Asp Leu Gln Asn Val Thr Leu Asn  
 515 520

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 850 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CTTTGGTTTT GAAGGAAGTA AGCGTGGACA ATTTGCTGTA GAAGGAATCA ATCAACTTCG	60
TGAGCATGTA GACACTCTAT TGATTATCTC AAACAACAAT TTGCTTGAAA TTGTTGATAA	120
GAAAACACCG CTTTGGAGG CTCTTAGCGA AGCGGATAAC GTTCTTCGTC AAGGTGTTCA	180
AGGGATTACC GATTTGATTA CCAATCCAGG ATTGATTAAC CTTGACTTTG CCGATGTGAA	240
AACGGTAATG GCAAACAAAG GGAATGCTCT TATGGGTATT GGTATCGGTA GTGGAGAAGA	300
ACGTGTGGTA GAAGCGGCAC GTAAGGCAAT CTATTCACCA CTTCTTGAAA CAACTATTGA	360
CGGTGCTGAG GATGTTATCG TCAACGTTAC TGGTGGTCTT GACTTAACCT TGATTGAGGC	420

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AGAAGAGGCT TCACAAATTG TGAACCAGGC AGCAGGTCAA GGAGTGAACA TCTGGCTCGG      480
TACTTCAATT GATGAAAGTA TGGGTGATGA AATTCGTGTA ACAGTTGTTG CAACGGGTGT      540
TCGTCAAGAC CGCGTAGAAA AGGTTGTGGC TCCACAAGCT AGATCTGCTA CTAAC TACCG      600
TGAGACAGTG AAACCAGCTC ATTCACATGG CTTTGATCGT CATTTTGATA TGGCAGAAAC      660
AGTTGAATTG CCAAAACAAA ATCCACGTCG TTTGGAACCA ACTCAGGCAT CTGCTTTTGG      720
TGATTGGGAT CTTGCGCGTG AATCGATTGT TCGTACAACA GATTCAGTCG TTTCTCCAGT      780
CGAGCGCTTT GAAGCCCCAA TTTCACAAGA TGAAGATGAA TTGGATACAC CTCCATTTTT      840
CAAAAATCGT                                     850

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## (2) INFORMATION FOR SEQ ID NO:124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:



```

Phe Gly Phe Glu Gly Ser Lys Arg Gly Gln Phe Ala Val Glu Gly Ile
1           5           10           15
Asn Gln Leu Arg Glu His Val Asp Thr Leu Leu Ile Ile Ser Asn Asn
20          25          30
Asn Leu Leu Glu Ile Val Asp Lys Lys Thr Pro Leu Leu Glu Ala Leu
35          40          45
Ser Glu Ala Asp Asn Val Leu Arg Gln Gly Val Gln Gly Ile Thr Asp
50          55          60
Leu Ile Thr Asn Pro Gly Leu Ile Asn Leu Asp Phe Ala Asp Val Lys
65          70          75          80
Thr Val Met Ala Asn Lys Gly Asn Ala Leu Met Gly Ile Gly Ile Gly
85          90          95
Ser Gly Glu Glu Arg Val Val Glu Ala Ala Arg Lys Ala Ile Tyr Ser
100         105         110
Pro Leu Leu Glu Thr Thr Ile Asp Gly Ala Glu Asp Val Ile Val Asn
115        120        125
Val Thr Gly Gly Leu Asp Leu Thr Leu Ile Glu Ala Glu Glu Ala Ser
130        135        140
Gln Ile Val Asn Gln Ala Ala Gly Gln Gly Val Asn Ile Trp Leu Gly
145        150        155        160
Thr Ser Ile Asp Glu Ser Met Arg Asp Glu Ile Arg Val Thr Val Val
165        170        175
Ala Thr Gly Val Arg Gln Asp Arg Val Glu Lys Val Val Ala Pro Gln

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180	185	190
Ala Arg Ser Ala Thr Asn Tyr Arg Glu Thr Val Lys Pro Ala His Ser		
195	200	205
His Gly Phe Asp Arg His Phe Asp Met Ala Glu Thr Val Glu Leu Pro		
210	215	220
Lys Gln Asn Pro Arg Arg Leu Glu Pro Thr Gln Ala Ser Ala Phe Gly		
225	230	235
Asp Trp Asp Leu Arg Arg Glu Ser Ile Val Arg Thr Thr Asp Ser Val		
245	250	255
Val Ser Pro Val Glu Arg Phe Glu Ala Pro Ile Ser Gln Asp Glu Asp		
260	265	270
Glu Leu Asp Thr Pro Pro Phe Phe Lys Asn Arg		
275	280	

## (2) INFORMATION FOR SEQ ID NO: 125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CTACTACCTC TCGAGAGAAA GTGACCTAGA GGTGACCGTT TTTGACCATG AGCAAGGTCA 60

AGCCACCAAG GCCGCAGCAG GAATTATCAG TCCTTGGTTT TCCAAACGCC GTAATAAAGC 120

CTGGTACAAG ATGGCGCGCT TGGGGGCTGA TTTTATGTG GATTTATTAG CTGATTTAGA 180

GAAATCAGGA CAAGAAATCG ACTTTTACCA GCGTTCGGGA GTCTTTCTCT TGAAAAAGGA 240

TGAATCCAAT TTGGAAGAAC TTTATCAACT GGCCCTCCAG CGCAGAGAAG AATCTCCCTT 300

GATAGGGCAA TTAGCCATTC TGAACCAAGC CTCAGCTAAT GAATTATTCC CTGGTTTGCA 360

GGGATTTGAC CGCCTGCTCT ATGCTTCTGG TGGAGCGAGA GTAGATGGCC AACTTTTAGT 420

GACTCGTTTG CTGGAAGTCA GTCATGTCAA GCTGGTCAAA GAAAAAGTGA CTCTGACACC 480

GTTAGCATCA GGCTACCAGA TTGGTGAAGA GGAGTTTGAG CAGGTTATTT TGGCGACGGG 540

AGCTTGGTTG GGGGACATGT TAGAGCCTTT AGGTTATGAA GTGGATGTCC GTCCTCAAAA 600

AGGACAAC TA CGAGATTATC AGCTTGCCCA AGACATGGAA GATTACCCTG TTGTCATGCC 660

AGAAGGGGAG TGGGATTTGA TTCCCTTTGC AGGTGGGAAA TTATCCTTAG GCGCTACCCA 720

CGAAAATGAC ATGGGATTTG ATTTGACGGT AGATGAAACC TTGCTCCAAC AAATGGAGGA 780

GGCCACCTTG ACTCACTATC TGATTTTGGC TGAAGCTACT TCAAAATCTG AGCGTGTTGG 840

AATCCGTGCC TACACCAAGT ATTTCTCTCC TTTCTTTGGG CAGGTGCCTG ACTTAACTGG 900

TGTCTATGCA GCCAGTGGAC TAGGTTTCATC AGGCCTCACA ACTGGTCCTA TCATTGGTTA 960

CCATCTAGCC CAACTGATCC AAGACAAGGA GTTGACCTTG GACCTCTAA ATTACCCAAT 1020

TGAAAACTAT GTCAAACGAG TAAAAAGCGA A 1051

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Tyr Tyr Leu Ser Arg Glu Ser Asp Leu Glu Val Thr Val Phe Asp His  
 1 5 10 15  
 Glu Gln Gly Gln Ala Thr Lys Ala Ala Ala Gly Ile Ile Ser Pro Trp  
 20 25 30  
 Phe Ser Lys Arg Arg Asn Lys Ala Trp Tyr Lys Met Ala Arg Leu Gly  
 35 40 45  
 Ala Asp Phe Tyr Val Asp Leu Leu Ala Asp Leu Glu Lys Ser Gly Gln  
 50 55 60  
 Glu Ile Asp Phe Tyr Gln Arg Ser Gly Val Phe Leu Leu Lys Lys Asp  
 65 70 75 80  
 Glu Ser Asn Leu Glu Glu Leu Tyr Gln Leu Ala Leu Gln Arg Arg Glu  
 85 90 95  
 Glu Ser Pro Leu Ile Gly Gln Leu Ala Ile Leu Asn Gln Ala Ser Ala  
 100 105 110  
 Asn Glu Leu Phe Pro Gly Leu Gln Gly Phe Asp Arg Leu Leu Tyr Ala  
 115 120 125  
 Ser Gly Gly Ala Arg Val Asp Gly Gln Leu Leu Val Thr Arg Leu Leu  
 130 135 140  
 Glu Val Ser His Val Lys Leu Val Lys Glu Lys Val Thr Leu Thr Pro  
 145 150 155 160  
 Leu Ala Ser Gly Tyr Gln Ile Gly Glu Glu Glu Phe Glu Gln Val Ile  
 165 170 175  
 Leu Ala Thr Gly Ala Trp Leu Gly Asp Met Leu Glu Pro Leu Gly Tyr  
 180 185 190  
 Glu Val Asp Val Arg Pro Gln Lys Gly Gln Leu Arg Asp Tyr Gln Leu  
 195 200 205  
 Ala Gln Asp Met Glu Asp Tyr Pro Val Val Met Pro Glu Gly Glu Trp  
 210 215 220  
 Asp Leu Ile Pro Phe Ala Gly Gly Lys Leu Ser Leu Gly Ala Thr His  
 225 230 235 240  
 Glu Asn Asp Met Gly Phe Asp Leu Thr Val Asp Glu Thr Leu Leu Gln  
 245 250 255

Gln	Met	Glu	Glu	Ala	Thr	Leu	Thr	His	Tyr	Leu	Ile	Leu	Ala	Glu	Ala
			260					265					270		
Thr	Ser	Lys	Ser	Glu	Arg	Val	Gly	Ile	Arg	Ala	Tyr	Thr	Ser	Asp	Phe
		275					280					285			
Ser	Pro	Phe	Phe	Gly	Gln	Val	Pro	Asp	Leu	Thr	Gly	Val	Tyr	Ala	Ala
	290					295					300				
Ser	Gly	Leu	Gly	Ser	Ser	Gly	Leu	Thr	Thr	Gly	Pro	Ile	Ile	Gly	Tyr
305					310					315					320
His	Leu	Ala	Gln	Leu	Ile	Gln	Asp	Lys	Glu	Leu	Thr	Leu	Asp	Pro	Leu
			325						330					335	
Asn	Tyr	Pro	Ile	Glu	Asn	Tyr	Val	Lys	Arg	Val	Lys	Ser	Glu		
			340					345					350		

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

TAAGGTCAA	AGTCAGACCG	CTAAGAAAAGT	GCTAGAAAAG	ATTGGAGCTG	ACTCGGTAT	60
CTCGCCAGAG	TATGAAATGG	GGCAGTCTCT	AGCACAGACC	ATTCTTTTCC	ATAATAGTGT	120
TGATGTCTTT	CAGTTGGATA	AAAATGTGTC	TATCGTGGAG	ATGAAAATTC	CTCAGTCTTG	180
GGCAGGTCAA	AGTCTGAGTA	AATTAGACCT	CCGTGGCAA	TACAATCTGA	ATATTTTGGG	240
TTTCCGAGAG	CAGGAAAATT	CCCCATTGGA	TGTTGAATTT	GGACCAGATG	ACCTCTTGAA	300
AGCAGATACC	TATATTTTGG	CAGTCATCAA	CAACCAGTAT	TTGGATACCC	TA	352

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Lys	Val	Lys	Ser	Gln	Thr	Ala	Lys	Lys	Val	Leu	Glu	Lys	Ile	Gly	Ala
1				5					10					15	
Asp	Ser	Val	Ile	Ser	Pro	Glu	Tyr	Glu	Met	Gly	Gln	Ser	Leu	Ala	Gln
			20					25					30		
Thr	Ile	Leu	Phe	His	Asn	Ser	Val	Asp	Val	Phe	Gln	Leu	Asp	Lys	Asn
		35					40					45			



Val Ser Ile Val Glu Met Lys Ile Pro Gln Ser Trp Ala Gly Gln Ser  
 50 55 60

Leu Ser Lys Leu Asp Leu Arg Gly Lys Tyr Asn Leu Asn Ile Leu Gly  
 65 70 75 80

Phe Arg Glu Gln Glu Asn Ser Pro Leu Asp Val Glu Phe Gly Pro Asp  
 85 90 95

Asp Leu Leu Lys Ala Asp Thr Tyr Ile Leu Ala Val Ile Asn Asn Gln  
 100 105 110

Tyr Leu Asp Thr Leu  
 115

## (2) INFORMATION FOR SEQ ID NO: 129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TGACGGGTCT CAGGATCAGA CTCAGGAAAT CGCTGAGTGT TTAGCTAGCA AGTATCCTAA 60

TATCGTTAGA GCCATCTATC AGGAAAATAA ATGCCATGGC GGTGCGGTCA ATCGTGGCTT 120

GGTAGAGGCT TCTGGGCGCT ATTTTAAAGT AGTTGACAGT GATGACTGGG TGGATCCTCG 180

TGCCTACTTG AAAATTCTTG AAACCTGCAG GAACTTGAGA GCAAAGGTCA AGAGGTGGAT 240

GTCTTTG 247

## (2) INFORMATION FOR SEQ ID NO:130:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Gly Ser Gln Asp Gln Thr Gln Glu Ile Ala Glu Cys Leu Ala Ser  
 1 5 10 15

Lys Tyr Pro Asn Ile Val Arg Ala Ile Tyr Gln Glu Asn Lys Cys His  
 20 25 30

Gly Gly Ala Val Asn Arg Gly Leu Val Glu Ala Ser Gly Arg Tyr Phe  
 35 40 45

Lys Val Val Asp Ser Asp Asp Trp Val Asp Pro Arg Ala Tyr Leu Lys  
 50 55 60

Ile Leu Glu Thr Cys Arg Asn Leu Arg Ala Lys Val Lys Arg Trp Met

65

70

75

80

Ser Leu

## (2) INFORMATION FOR SEQ ID NO: 131:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1744 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

TAGAGGCTTT GCCAAATGGT GGGAAGGGCA CGAGCGTCGA AAAGAGGAAC GCTTTGTCAA 60  
 ACAAGAAGAA AAAGCTCGCC AAAAGGCTGA GAAAGAGGCT AGATTAGAAC AAGAAGAGAC 120  
 TGAAAAAGCC TTACTCGATT TGCCTCCTGT TGATATGGAA ACGGGTGAAA TTC'TGACAGA 180  
 GGAAGCTGTT CAAAATCTTC CACCTATTCC AGAAGAAAAG TGGGTGGAAC CAGAAATCAT 240  
 CCTGCCTCAA GCTGAACTTA AAT'TCCCTGA ACAGGAAGAT GACTCAGATG ACGAAGATGT 300  
 TCAGGTCGAT TTTTCAGCCA AAGAAGCCCT TGAATACAAA C'TTCCAAGCT TACAAC'TCTT 360  
 TGCACCAGAT AAACCAAAAG ATCAGTCTAA AGAGAAGAAA ATTGTCAGAG AAAATATCAA 420  
 AATCTTAGAA GCAACCTTTG CTAGCTTTGG TATTAAGGTA ACAGTTGAAC GGGCCGAAAT 480  
 TGGGCCATCA GTGACCAAGT ATGAAGTCAA GCCGGCTGTT GGTGTAAGGG TCAACCGCAT 540  
 TTCCAATCTA TCAGATGACC TCGCTCTAGC CTTGGCTGCC AAAGATGTCC GGATTGAAGC 600  
 ACCAATCCCT GGGAAATCCC TAATCGGAAT TGAAGTGCCC AACTCCGATA TTGCCACTGT 660  
 ATCTTTCCGA GAACTATGGG AACAATCGCA AACGAAAGCA GAAAATTTCT TGGAAATTCC 720  
 TTTAGGGAAG GCTGTTAATG GAACCGCAAG AGCTTTTGAC CTTTCTAAAA TGCCCCACTT 780  
 GCTAGTTGCA GGTTCACGG GTTCAGGGAA GTCAGTAGCA GTTAACGGCA TTATTGCTAG 840  
 CATTCATG AAGGCGAGAC CAGATCAAGT TAAATTTATG ATGGTCGATC CCAAGATGGT 900  
 TGAGTTATCT GTTTACAATG ATATTCCCCA CCTCTTGATT CCAGTCGTGA CCAATCCACG 960  
 CAAAGCCAGC AAGGCTCTGC AAAAGGTTGT GGATGAAATG GAAAACCGTT ATGAACTCTT 1020  
 TGCCAAGGTG GGAGTTCGGA ATATTGCAGG TTTTAATGCC AAGGTAGAAG AGTTCAATTC 1080  
 CCAGTCTGAG TACAAGCAAA TTCCGCTACC ATTCAATTGTC GTGATTGTGG ATGAGTTGGC 1140  
 TGACCTCATG ATGGTGGCCA GCAAGGAAGT GGAAGATGCT ATCATCCGTC TTGGGCAGAA 1200  
 GCGCGTGCT GCAGGTATCC ACATGATTCT TGCAACTCAG CGTCCATCTG TTGATGTCAT 1260  
 CTCTGGTTTG ATTAAGGCCA ATGTTCCATC TCGTGTAGCA TTTGCGGTTT CATCAGGAAC 1320  
 AGACTCCCGT ACGATTTTGG ATGAAAATGG AGCAGAAAAA CTTCTTGGTC GAGGAGACAT 1380  
 GCTCTTTAAA CCGATTGATG AAAATCATCC AGTTCGTCTC CAAGGCTCCT TTATCTCGGA 1440

TGACGATGTT GAGCGCATTG TGAAC TTCAT CAAGACTCAG GCAGATGCAG ACTACGATGA 1500  
 GAGTTTTGAT CCAGGTGAGG TTTCTGAAAA TGAAGGAGAA TTTTCGGATG GAGATGCTGG 1560  
 TGGTGATCCG CTTTTTGAAG AAGCTAAGTC TTTGGTTATC GAAACACAGA AAGCCAGTGC 1620  
 GTCTATGATT CAGCGTCGTT TATCAGTTGG ATTTAACCGT GCGACCCGTC TCATGGAAGA 1680  
 ACTGGAGATA GCAGGTGTCA TCGGTCCAGC TGAAGGTACC AAACCTCGAA AAGTGTTACA 1740  
 ACAA 1744

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Arg Gly Phe Ala Lys Trp Trp Glu Gly His Glu Arg Arg Lys Glu Glu  
 1 5 10 15  
 Arg Phe Val Lys Gln Glu Glu Lys Ala Arg Gln Lys Ala Glu Lys Glu  
 20 25 30  
 Ala Arg Leu Glu Gln Glu Glu Thr Glu Lys Ala Leu Leu Asp Leu Pro  
 35 40 45  
 Pro Val Asp Met Glu Thr Gly Glu Ile Leu Thr Glu Glu Ala Val Gln  
 50 55 60  
 Asn Leu Pro Pro Ile Pro Glu Glu Lys Trp Val Glu Pro Glu Ile Ile  
 65 70 75 80  
 Leu Pro Gln Ala Glu Leu Lys Phe Pro Glu Gln Glu Asp Asp Ser Asp  
 85 90 95  
 Asp Glu Asp Val Gln Val Asp Phe Ser Ala Lys Glu Ala Leu Glu Tyr  
 100 105 110  
 Lys Leu Pro Ser Leu Gln Leu Phe Ala Pro Asp Lys Pro Lys Asp Gln  
 115 120 125  
 Ser Lys Glu Lys Lys Ile Val Arg Glu Asn Ile Lys Ile Leu Glu Ala  
 130 135 140  
 Thr Phe Ala Ser Phe Gly Ile Lys Val Thr Val Glu Arg Ala Glu Ile  
 145 150 155 160  
 Gly Pro Ser Val Thr Lys Tyr Glu Val Lys Pro Ala Val Gly Val Arg  
 165 170 175  
 Val Asn Arg Ile Ser Asn Leu Ser Asp Asp Leu Ala Leu Ala Leu Ala  
 180 185 190  
 Ala Lys Asp Val Arg Ile Glu Ala Pro Ile Pro Gly Lys Ser Leu Ile  
 195 200 205

Gly Ile Glu Val Pro Asn Ser Asp Ile Ala Thr Val Ser Phe Arg Glu  
 210 215 220  
 Leu Trp Glu Gln Ser Gln Thr Lys Ala Glu Asn Phe Leu Glu Ile Pro  
 225 230 235 240  
 Leu Gly Lys Ala Val Asn Gly Thr Ala Arg Ala Phe Asp Leu Ser Lys  
 245 250 255  
 Met Pro His Leu Leu Val Ala Gly Ser Thr Gly Ser Gly Lys Ser Val  
 260 265 270  
 Ala Val Asn Gly Ile Ile Ala Ser Ile Leu Met Lys Ala Arg Pro Asp  
 275 280 285  
 Gln Val Lys Phe Met Met Val Asp Pro Lys Met Val Glu Leu Ser Val  
 290 295 300  
 Tyr Asn Asp Ile Pro His Leu Leu Ile Pro Val Val Thr Asn Pro Arg  
 305 310 315 320  
 Lys Ala Ser Lys Ala Leu Gln Lys Val Val Asp Glu Met Glu Asn Arg  
 325 330 335  
 Tyr Glu Leu Phe Ala Lys Val Gly Val Arg Asn Ile Ala Gly Phe Asn  
 340 345 350  
 Ala Lys Val Glu Glu Phe Asn Ser Gln Ser Glu Tyr Lys Gln Ile Pro  
 355 360 365  
 Leu Pro Phe Ile Val Val Ile Val Asp Glu Leu Ala Asp Leu Met Met  
 370 375 380  
 Val Ala Ser Lys Glu Val Glu Asp Ala Ile Ile Arg Leu Gly Gln Lys  
 385 390 395 400  
 Ala Arg Ala Ala Gly Ile His Met Ile Leu Ala Thr Gln Arg Pro Ser  
 405 410 415  
 Val Asp Val Ile Ser Gly Leu Ile Lys Ala Asn Val Pro Ser Arg Val  
 420 425 430  
 Ala Phe Ala Val Ser Ser Gly Thr Asp Ser Arg Thr Ile Leu Asp Glu  
 435 440 445  
 Asn Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp Met Leu Phe Lys Pro  
 450 455 460  
 Ile Asp Glu Asn His Pro Val Arg Leu Gln Gly Ser Phe Ile Ser Asp  
 465 470 475 480  
 Asp Asp Val Glu Arg Ile Val Asn Phe Ile Lys Thr Gln Ala Asp Ala  
 485 490 495  
 Asp Tyr Asp Glu Ser Phe Asp Pro Gly Glu Val Ser Glu Asn Glu Gly  
 500 505 510  
 Glu Phe Ser Asp Gly Asp Ala Gly Gly Asp Pro Leu Phe Glu Glu Ala  
 515 520 525  
 Lys Ser Leu Val Ile Glu Thr Gln Lys Ala Ser Ala Ser Met Ile Gln  
 530 535 540

Arg Arg Leu Ser Val Gly Phe Asn Arg Ala Thr Arg Leu Met Glu Glu  
545 550 555 560

Leu Glu Ile Ala Gly Val Ile Gly Pro Ala Glu Gly Thr Lys Pro Arg  
565 570 575

Lys Val Leu Gln Gln  
580

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

TCAAAAAGAG AAGGAAACT TGGTTATTGC TGGGAAAATA GGTCCAGAAC CAGAAATTTT 60  
GGCCAATATG TATAAGTTGC TGATTGAAGA AAATACCAGC ATGACTGCGA CTGTTAAACC 120  
GAATTTTGGG AAGACAAGCT TCCTTTATGA AGCTCTGAAA AAAGGCGATA TTGACATCTA 180  
TCCTGAATTT ACTGGTACGG TGAAGTAAAG TTTGCTTCAA CCATCACCCA AGGTGAGTCA 240  
TGAACCAGAA CAGGTTTATC AGGTGGCGCG TGATGGCATT GCTAAGCAGG ATCATCTAGC 300  
CTATCTCAAA CCCATGTCTT ATCAAAACAC CTATGCTGTA GCTGTTCCGA AAAAGATTGC 360  
TCAAGAATAT GGCTTGAAGA CCATTTTCTA CTTGAAAAAA GTGGAAGGGC AGTTGAAGGC 420  
AGGTTTTTACA CTCGAGTTTA ACGACCGTGA AGATGGAAAT AAGGGCTTGC AATCAATGTA 480  
TGGTCTCAAT CTCAATGTAG CGACCATTGA GCCAGCCCTT CGCTATCAGG CTATTCAGTC 540  
AGGGGATATT CAAATCACGG ATGCCTATTC GACTGATGCG GAATTGGAGC GTTATGATTT 600  
ACAGGTCTTG GAAGATGACA AGCAACTCTT CCCACCTTAT CAAGGGGCTC CACTCATGAA 660  
AGAAGCTCTT CTCAAGAAAC ACCCAGAGTT GGAAAGAGTT CTTAATACAT TGGCTGGTAA 720  
GATTACAGAA AGCCAGATGA GCCAGCTCAA CTACCAAGTC GGTGTTGAAG GCAAGTCAGC 780  
AAAGCAAGTA GCCAAGGAGT TTCTCCAAGA ACAAGGTTTG TTGAAGAAA 829

(2) INFORMATION FOR SEQ ID NO:134:


(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Gln Lys Glu Lys Glu Asn Leu Val Ile Ala Gly Lys Ile Gly Pro Glu  
1 5 10 15



Pro Glu Ile Leu Ala Asn Met Tyr Lys Leu Leu Ile Glu Glu Asn Thr  
 20 25 30  
 Ser Met Thr Ala Thr Val Lys Pro Asn Phe Gly Lys Thr Ser Phe Leu  
 35 40 45  
 Tyr Glu Ala Leu Lys Lys Gly Asp Ile Asp Ile Tyr Pro Glu Phe Thr  
 50 55 60  
 Gly Thr Val Thr Glu Ser Leu Leu Gln Pro Ser Pro Lys Val Ser His  
 65 70 75 80  
 Glu Pro Glu Gln Val Tyr Gln Val Ala Arg Asp Gly Ile Ala Lys Gln  
 85 90 95  
 Asp His Leu Ala Tyr Leu Lys Pro Met Ser Tyr Gln Asn Thr Tyr Ala  
 100 105 110  
 Val Ala Val Pro Lys Lys Ile Ala Gln Glu Tyr Gly Leu Lys Thr Ile  
 115 120 125  
 Ser Asp Leu Lys Lys Val Glu Gly Gln Leu Lys Ala Gly Phe Thr Leu  
 130 135 140  
 Glu Phe Asn Asp Arg Glu Asp Gly Asn Lys Gly Leu Gln Ser Met Tyr  
 145 150 155 160  
 Gly Leu Asn Leu Asn Val Ala Thr Ile Glu Pro Ala Leu Arg Tyr Gln  
 165 170 175  
 Ala Ile Gln Ser Gly Asp Ile Gln Ile Thr Asp Ala Tyr Ser Thr Asp  
 180 185 190  
 Ala Glu Leu Glu Arg Tyr Asp Leu Gln Val Leu Glu Asp Asp Lys Gln  
 195 200 205  
 Leu Phe Pro Pro Tyr Gln Gly Ala Pro Leu Met Lys Glu Ala Leu Leu  
 210 215 220  
 Lys Lys His Pro Glu Leu Glu Arg Val Leu Asn Thr Leu Ala Gly Lys  
 225 230 235 240  
 Ile Thr Glu Ser Gln Met Ser Gln Leu Asn Tyr Gln Val Gly Val Glu  
 245 250 255  
 Gly Lys Ser Ala Lys Gln Val Ala Lys Glu Phe Leu Gln Glu Gln Gly  
 260 265 270  
 Leu Leu Lys Lys  
 275

## (2) INFORMATION FOR SEQ ID NO: 135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 712 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

ACGTTCTATT GAGGACCACT TTGATTCAAA CTTCGAATTG GAATATAACC TCAAAGAAAA 60  
 AGGGAAAACA GATCTTTTGA AGCTAGTTGA TAAACAACCT GACATGCGTC TGCATTTTAT 120  
 CCGCCAAACT CATCCACGCG GTCTCGGAGA TGCTGTTTTG CAAGCCAAGG CTTTCGTCGG 180  
 AAATGAACCT TTTGTCGTTA TGCTTGGTGA TGACTTGATG GATATCACAG ACGAAAAGGC 240  
 TGTTCCACTT ACCAAACAAC TCATGGATGA CTACGAGCGT ACCCAGCGCT CTACTATCGC 300  
 TGTCATGCCA GTCCCTCATG ACGAAGTATC TGCTTACGGG GTTATTGCTC CGCAAGGCGA 360  
 AGGAAAAGAT GGTCTTTTACA GTGTTGAAAC CTTTGTGTA AAACCAGCTC CAGAGGACGC 420  
 TCCTAGCGAC CTTGCTATTA TCGGACGCTA CCTCCTCACG CCTGAAATTT TTGAGATTCT 480  
 CGAAAAGCAA GCTCCAGGTG CAGGAAATGA AATTCAGCTG ACAGATGCAA TCGACACCCT 540  
 CAATAAAACA CAACGTGTAT TTGCTCGTGA GTTCAAAGGG GCTCGTTACG ATGTCGGAGA 600  
 CAAGTTTGGC TTCATGAAAA CATCCATCGA CTACGCCCTC AACACCCAC AAGTCAAAGA 660  
 TGATTTGAAG AATTACCTCA TCCAAC TTGG AAAAGAATTG ACTGAGAAGG AA 712

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Arg Ser Ile Glu Asp His Phe Asp Ser Asn Phe Glu Leu Glu Tyr Asn  
 1 5 10 15  
 Leu Lys Glu Lys Gly Lys Thr Asp Leu Leu Lys Leu Val Asp Lys Thr  
 20 25 30  
 Thr Asp Met Arg Leu His Phe Ile Arg Gln Thr His Pro Arg Gly Leu  
 35 40 45  
 Gly Asp Ala Val Leu Gln Ala Lys Ala Phe Val Gly Asn Glu Pro Phe  
 50 55 60  
 Val Val Met Leu Gly Asp Asp Leu Met Asp Ile Thr Asp Glu Lys Ala  
 65 70 75 80  
 Val Pro Leu Thr Lys Gln Leu Met Asp Asp Tyr Glu Arg Thr His Ala  
 85 90 95  
 Ser Thr Ile Ala Val Met Pro Val Pro His Asp Glu Val Ser Ala Tyr  
 100 105 110  
 Gly Val Ile Ala Pro Gln Gly Glu Gly Lys Asp Gly Leu Tyr Ser Val  
 115 120 125  
 Glu Thr Phe Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Asp Leu  
 130 135 140

Ala Ile Ile Gly Arg Tyr Leu Leu Thr Pro Glu Ile Phe Glu Ile Leu  
 145 150 155 160  
 Glu Lys Gln Ala Pro Gly Ala Gly Asn Glu Ile Gln Leu Thr Asp Ala  
 165 170 175  
 Ile Asp Thr Leu Asn Lys Thr Gln Arg Val Phe Ala Arg Glu Phe Lys  
 180 185 190  
 Gly Ala Arg Tyr Asp Val Gly Asp Lys Phe Gly Phe Met Lys Thr Ser  
 195 200 205  
 Ile Asp Tyr Ala Leu Lys His Pro Gln Val Lys Asp Asp Leu Lys Asn  
 210 215 220  
 Tyr Leu Ile Gln Leu Gly Lys Glu Leu Thr Glu Lys Glu  
 225 230 235

## (2) INFORMATION FOR SEQ ID NO: 137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CGCTCAAAAT ACCAGAGGTG TTCAGCTAAT CGAGCACGTT TCTCCTCAAA TGTTGAAAGC 60  
 CCAATTGGAG AGTGTCTTTT CTGATATTCC ACCTCAGGCT GTAAAACTG GAATGTTGGC 120  
 TACTACTGAA ATCATGGAAA TCATCCAACC CTATCTTAAA AACTGGATT GTCCCTATGT 180  
 CCTTGATCCT GTTATGGTTG CTACAAGTGG AGATGCCCTTG ATTGACTCAA ATGCTAGAGA 240  
 CTATCTCAAA ACAAACTTAC TACCTCTAGC AACTATTATT ACGCCAAATC TTCCTGAAGC 300  
 AGAAGAGATT GTTGGTTTTT CAATCCATGA CCCCAGAGAC ATGCAGCGTG CTGGTCGCCT 360  
 GATTTTAAAA GAATTTGGTC CTCAGTCTGT GGTATCAAAA GGCGGACATC TCAAAGGTGG 420  
 TGCTAAAGAT TTCCTCTTTA CCAAGAATGA ACAATTTGTC TGGGAAAGCC CACGAATTCA 480  
 AACCTGTCAC ACCCATGGTA CT 502

## (2) INFORMATION FOR SEQ ID NO:138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ala Gln Asn Thr Arg Gly Val Gln Leu Ile Glu His Val Ser Pro Gln  
 1 5 10 15



Met Leu Lys Ala Gln Leu Glu Ser Val Phe Ser Asp Ile Pro Pro Gln  
 20 25 30

Ala Val Lys Thr Gly Met Leu Ala Thr Thr Glu Ile Met Glu Ile Ile  
 35 40 45

Gln Pro Tyr Leu Lys Lys Leu Asp Cys Pro Tyr Val Leu Asp Pro Val  
 50 55 60

Met Val Ala Thr Ser Gly Asp Ala Leu Ile Asp Ser Asn Ala Arg Asp  
 65 70 75 80

Tyr Leu Lys Thr Asn Leu Leu Pro Leu Ala Thr Ile Ile Thr Pro Asn  
 85 90 95

Leu Pro Glu Ala Glu Glu Ile Val Gly Phe Ser Ile His Asp Pro Glu  
 100 105 110

Asp Met Gln Arg Ala Gly Arg Leu Ile Leu Lys Glu Phe Gly Pro Gln  
 115 120 125

Ser Val Val Ile Lys Gly Gly His Leu Lys Gly Gly Ala Lys Asp Phe  
 130 135 140

Leu Phe Thr Lys Asn Glu Gln Phe Val Trp Glu Ser Pro Arg Ile Gln  
 145 150 155 160

Thr Cys His Thr His Gly Thr  
 165

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

AATTGTACAA TTAGAAAAAG ATAGCAAATC AGACAAAGAA CAAGTTGATA AACTATTTGA	60
ATCATTTGAT GCATCTTCAG ATGAATCTAT TTCTAAATTA AAAGAACTAT CTGAAACTTC	120
ACTTAAAACC GATGCAGGTA AAGACTATCT TAATAACAAA GTCAAAGAAT CATCTAAAGC	180
AATTGTAGAT TTTCATTTGC AAAAAGGTTT GGCTTATGAT GTTAAAGATT CAGATGACAA	240
ATTTAAAGAT AAAGCAACTC TTGAAACAAA TGTAAGAGAA ATTACAAAAC AAATTGATTT	300
TATCAAAAAA GTTGATGAAA CTTTAAACA AGAGAATTTG GAAGAACTC TTAAATCTCT	360
AAATGATCTT GTTGATAAAT ATCAAAAACA AATCGAACTT TTGAAGAAAG AAGAAGAAAA	420
AGCTGCTGAA AAAGCTGCTG AAAAAGCAAA GGAATCTTCT AGTCAAAGTA ATCTTCTG	480
TAGTGCTTCT AATGAGTCTT ATAATGGATC TTCCAATTCA AATGTAGATT ATAGTTCATC	540
TGAACAACT AATGGATATT CAAATAATTA TGGCGGTCAA GATTATTCTG GTTCAGGAGA	600
TAGTTCAACA AATGGTGGAT CATCAGAACA ATATTCATCT AGCAATTCAA ACAGCGGAGC	660

AAATAATGTC TACAGATATA AAGGCACTGG TGCTGACGGC TATCAAAGAT ACTACTACAA 720  
 AGATCATAAT AATGGAGATG TGTATGATGA CGATGGAAAT TACCTTGGGA ACTTTGGTGG 780  
 CGGCATTGCA GAACCTAGTC AACGC 805

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ile Val Gln Leu Glu Lys Asp Ser Lys Ser Asp Lys Glu Gln Val Asp  
 1 5 10 15  
 Lys Leu Phe Glu Ser Phe Asp Ala Ser Ser Asp Glu Ser Ile Ser Lys  
 20 25 30  
 Leu Lys Glu Leu Ser Glu Thr Ser Leu Lys Thr Asp Ala Gly Lys Asp  
 35 40 45  
 Tyr Leu Asn Asn Lys Val Lys Glu Ser Ser Lys Ala Ile Val Asp Phe  
 50 55 60  
 His Leu Gln Lys Gly Leu Ala Tyr Asp Val Lys Asp Ser Asp Asp Lys  
 65 70 75 80  
 Phe Lys Asp Lys Ala Thr Leu Glu Thr Asn Val Lys Glu Ile Thr Lys  
 85 90 95  
 Gln Ile Asp Phe Ile Lys Lys Val Asp Glu Thr Phe Lys Gln Glu Asn  
 100 105 110  
 Leu Glu Glu Thr Leu Lys Ser Leu Asn Asp Leu Val Asp Lys Tyr Gln  
 115 120 125  
 Lys Gln Ile Glu Leu Leu Lys Lys Glu Glu Glu Lys Ala Ala Glu Lys  
 130 135 140  
 Ala Ala Glu Lys Ala Lys Glu Ser Ser Ser Gln Ser Asn Ser Ser Gly  
 145 150 155 160  
 Ser Ala Ser Asn Glu Ser Tyr Asn Gly Ser Ser Asn Ser Asn Val Asp  
 165 170 175  
 Tyr Ser Ser Ser Glu Gln Thr Asn Gly Tyr Ser Asn Asn Tyr Gly Gly  
 180 185 190  
 Gln Asp Tyr Ser Gly Ser Gly Asp Ser Ser Thr Asn Gly Gly Ser Ser  
 195 200 205  
 Glu Gln Tyr Ser Ser Ser Asn Ser Asn Ser Gly Ala Asn Asn Val Tyr  
 210 215 220  
 Arg Tyr Lys Gly Thr Gly Ala Asp Gly Tyr Gln Arg Tyr Tyr Tyr Lys  
 225 230 235 240

Asn Phe Gly Gly Gly Ile Ala Glu Pro Ser Gln Arg  
260 265

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 211 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TCTGACCAAG	CAAAAAAGAAG	CAGTCAATGA	CAAAGGAAAA	GCAGCTGTTG	TTAAGGTGGT	60
GGAAAGCCAG	GCAGAACTTT	ATAGCTTAGA	AAAGAATGAA	GATGCTAGCC	TAAGAAAGTT	120
ACAAGCAGAT	GGACGCATCA	CGGAAGAACA	GGCTAAAGCT	TATAAAGAAT	ACAATGATAA	180
AAATGGAGGA	GCAAAATCGTA	AAGTCAATGA	T			211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

[illegible]

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC GGTAGAGGAA CAGATTTTCT TTATGGAGTT 60  
TGAAGAAGTC TATCGGGAAA CCCAAAAACG CAGTGTAGCC AGTCAGCAA AGACTAGTCT 120  
GAACCTTAGAT GGGCAGACGC TTAGCAATGG CAGTCAAAAG TTGCCAGTCC CTAAAGGAAT 180  
TCAGGCCCCA TCAGGCCAAA GTATTACATT TGACCGAGCT GGGGGCAATT CGTCCCTGGC 240  
TAAGGTTGAA TTTCAGACCA GTAAAGGAGC GATTGCTAT CAATTATATC TAGGAAATGG 300  
AAAAATTAAA CGCATTAAGG AAACAAAAAA T 331

## (2) INFORMATION FOR SEQ ID NO:144:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Ser Gly Ser Val Gln Ser Thr Phe Ser Ala Val Glu Glu Gln Ile Phe  
1 5 10 15  
Phe Met Glu Phe Glu Glu Leu Tyr Arg Glu Thr Gln Lys Arg Ser Val  
20 25 30  
Ala Ser Gln Gln Lys Thr Ser Leu Asn Leu Asp Gly Gln Thr Leu Ser  
35 40 45  
Asn Gly Ser Gln Lys Leu Pro Val Pro Lys Gly Ile Gln Ala Pro Ser  
50 55 60  
Gly Gln Ser Ile Thr Phe Asp Arg Ala Gly Gly Asn Ser Ser Leu Ala  
65 70 75 80  
Lys Val Glu Phe Gln Thr Ser Lys Gly Ala Ile Arg Tyr Gln Leu Tyr  
85 90 95  
Leu Gly Asn Gly Lys Ile Lys Arg Ile Lys Glu Thr Lys Asn  
100 105 110

## (2) INFORMATION FOR SEQ ID NO: 145:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

GGGACAAATT CAAAAAATA GGCAAGAGGA AGCAAAATC TTGCAAAAGG AAGAAGTCTT 60  
GAGGGTAGCT AAGATGGCCC TGCAGACGGG GCAAAATCAG GTAAGCATCA ACGGAGTTGA 120

GATTCAGGTA TTTTCTAGTG AAAAAGGATT GGAGGTCTAC CATGGTTCAG AACAGTTGTT 180  
GGCAATCAAA GAGCCA 196

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Gly Gln Ile Gln Lys Asn Arg Gln Glu Glu Ala Lys Ile Leu Gln Lys  
1 5 10 15  
Glu Glu Val Leu Arg Val Ala Lys Met Ala Leu Gln Thr Gly Gln Asn  
20 25 30  
Gln Val Ser Ile Asn Gly Val Glu Ile Gln Val Phe Ser Ser Glu Lys  
35 40 45  
Gly Leu Glu Val Tyr His Gly Ser Glu Gln Leu Leu Ala Ile Lys Glu  
50 55 60  
Pro  
65

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 319 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

TCGCTACCAG CAACAAAGCG AGCAAAAGGA GTGGCTCTTG TTTGTGGACC AACTTGAGGT 60  
AGAATTAGAC CGTTCGCAGT TCGAAAAAGT AGAAGGCAAT CGCCTATACA TGAAGCAAGA 120  
TGGCAAGGAC ATCGCCATCG GTAAGTCAAA GTCAGATGAT TTCCGTAAAA CGAATGCTCG 180  
TGGTCGAGGT TATCAGCCTA TGGTTTATGG ACTCAAATCT GTACGGATTA CAGAGGACAA 240  
TCAACTGGTT CGCTTTCATT TCCAGTTCCA AAAAGGCTTA GAAAGGGAGT TCATCTATCG 300  
TGTGGAAAAA GAAAAAAGT 319

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```

Arg Tyr Gln Gln Gln Ser Glu Gln Lys Glu Trp Leu Leu Phe Val Asp
1          5          10          15
Gln Leu Glu Val Glu Leu Asp Arg Ser Gln Phe Glu Lys Val Glu Gly
20          25          30
Asn Arg Leu Tyr Met Lys Gln Asp Gly Lys Asp Ile Ala Ile Gly Lys
35          40          45
Ser Lys Ser Asp Asp Phe Arg Lys Thr Asn Ala Arg Gly Arg Gly Tyr
50          55          60
Gln Pro Met Val Tyr Gly Leu Lys Ser Val Arg Ile Thr Glu Asp Asn
65          70          75          80
Gln Leu Val Arg Phe His Phe Gln Phe Gln Lys Gly Leu Glu Arg Glu
85          90          95
Phe Ile Tyr Arg Val Glu Lys Glu Lys Ser
100          105

```

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```

GAACCGACAA GTCGCCCACT ATCAAGACTA TGCTTTGAAT AAAGAAAAAT TGGTTGCTTT      60
TGCTATGGCT AAACGAACCA AAGATAAGGT TGAGCAAGAA AGTGGGGAAC AGTTTTTTTAA      120
TCTAGGTCAG GTAAGCTATC AAAACAAGAA AACTGGCTTA GTGACGAGGG TTCGTACGGA      180
TAAGAGCCAA TATGAGTTTC TGTTTCCTTC AGTCAAAATC AAAGAAGAGA AAAGAGATAA      240
AAAGGAAGAG GTAGCGACCG ATTCAAGCGA AAAAGTGGAG AAGAAAAAAT CAGAAGAGAA      300
GCCTGAAAAG AAAGAGAATT CA                                          322

```

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

Asn Arg Gln Val Ala His Tyr Gln Asp Tyr Ala Leu Asn Lys Glu Lys

```

1	5	10	15
Leu Val Ala Phe Ala Met Ala Lys Arg Thr Lys Asp Lys Val Glu Gln	20	25	30
Glu Ser Gly Glu Gln Phe Phe Asn Leu Gly Gln Val Ser Tyr Gln Asn	35	40	45
Lys Lys Thr Gly Leu Val Thr Arg Val Arg Thr Asp Lys Ser Gln Tyr	50	55	60
Glu Phe Leu Phe Pro Ser Val Lys Ile Lys Glu Glu Lys Arg Asp Lys	65	70	75
Lys Glu Glu Val Ala Thr Asp Ser Ser Glu Lys Val Glu Lys Lys Lys	85	90	95
Ser Glu Glu Lys Pro Glu Lys Lys Glu Asn Ser	100	105	

## (2) INFORMATION FOR SEQ ID NO: 151:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

GGTTGTCGGC TGGCAATATA TCCCGTTTCC ATCTAAAGGT AGTACAATTG GTCCTTACCC 60  
 AAATGGTATC AGATTAGAAG GTTTTCCAAA GTCAGAGTGG TACTACTTCG ATAAAAATGG 120  
 AGTGCTACAA GAGTTTGTGT GTTGGAAGAAC ATTAGAGATT AAAACTAAAG ACAGTGTTGG 180  
 AAGAAAGTAC GGGGAAAAAC GTGAAGATTC AGAAGATAAA GAAGAGAAGC GTTATTATAC 240  
 GAACTATTAC TTTAATCAAA ATCATTCCTT AGAGACAGGT TGGCTTTATG ATCAGTCTAA 300  
 CTGGTATTAT CTAGCTAAGA CGGAAATTAA TGGAGAAAAC TACCTTGGTG GTGAAAGACG 360  
 TGCGGGGTGG ATAAACGATG ATTCGACTTG GTACTACCTA GATCCAACAA CTGGTATTAT 420  
 GCAAACAGGT TGGCAATATC TAGGTAATAA GTGGTACTAC CTCCGTTCCCT CAGGAGCAAT 480  
 GGCCACTGGC TGGTATCAGG AAGGTACCAC TTGGTATTAT TTAGACCACC CAAATGGCGA 540  
 TATGAAAACA GGTGGAACA ACCTTGGGAA CAAATGGTAC TATCTCCGTT CATCAGGAGC 600  
 TATGGCAACT GGTGATATC AAGATGGTTC AACTTGGTAC TACCTAAATG CAGGTAATGG 660  
 AGACATGAAG ACAGGTTGGT TCCAGGTCAA TGGCAACTGG TACTATGCTT ATAGCTCAGG 720  
 TGCTTTGGCA GTGAATACGA CCGTAGATGG CTATTCTGTC AACTATAATG GCGAATGGGT 780  
 TCGG 784

## (2) INFORMATION FOR SEQ ID NO:152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Val Val Gly Trp Gln Tyr Ile Pro Phe Pro Ser Lys Gly Ser Thr Ile  
 1 5 10 15  
 Gly Pro Tyr Pro Asn Gly Ile Arg Leu Glu Gly Phe Pro Lys Ser Glu  
 20 25 30  
 Trp Tyr Tyr Phe Asp Lys Asn Gly Val Leu Gln Glu Phe Val Gly Trp  
 35 40 45  
 Lys Thr Leu Glu Ile Lys Thr Lys Asp Ser Val Gly Arg Lys Tyr Gly  
 50 55 60  
 Glu Lys Arg Glu Asp Ser Glu Asp Lys Glu Glu Lys Arg Tyr Tyr Thr  
 65 70 75 80  
 Asn Tyr Tyr Phe Asn Gln Asn His Ser Leu Glu Thr Gly Trp Leu Tyr  
 85 90 95  
 Asp Gln Ser Asn Trp Tyr Tyr Leu Ala Lys Thr Glu Ile Asn Gly Glu  
 100 105 110  
 Asn Tyr Leu Gly Gly Glu Arg Arg Ala Gly Trp Ile Asn Asp Asp Ser  
 115 120 125  
 Thr Trp Tyr Tyr Leu Asp Pro Thr Thr Gly Ile Met Gln Thr Gly Trp  
 130 135 140  
 Gln Tyr Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met  
 145 150 155 160  
 Ala Thr Gly Trp Tyr Gln Glu Gly Thr Thr Trp Tyr Tyr Leu Asp His  
 165 170 175  
 Pro Asn Gly Asp Met Lys Thr Gly Trp Gln Asn Leu Gly Asn Lys Trp  
 180 185 190  
 Tyr Tyr Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Asp  
 195 200 205  
 Gly Ser Thr Trp Tyr Tyr Leu Asn Ala Gly Asn Gly Asp Met Lys Thr  
 210 215 220  
 Gly Trp Phe Gln Val Asn Gly Asn Trp Tyr Tyr Ala Tyr Ser Ser Gly  
 225 230 235 240  
 Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Ser Val Asn Tyr Asn  
 245 250 255  
 Gly Glu Trp Val Arg  
 260

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1708 base pairs



(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

GGCCAAATCA	GAATGGGTAG	AAGACAAGGG	AGCCTTTTAT	TATCTTGACC	AAGATGGAAA	60
GATGAAAAGA	AATGCTTGGG	TAGGAAC TTC	CTATGTTGGT	GCAACAGGTG	CCAAAGTAAT	120
AGAAGACTGG	GTCTATGATT	CTCAATACGA	TGCTTGGTTT	TATATCAAAG	CAGATGGACA	180
GCACGCAGAG	AAAGAATGGC	TCCAAAT TAA	AGGGAAGGAC	TATTATTTCA	AATCCGGTGG	240
TTATCTACTG	ACAAGTCAGT	GGATTAATCA	AGCTTATGTG	AATGCTAGTG	GTGCCAAAGT	300
ACAGCAAGGT	TGGCTTTTTG	ACAAACAATA	CCAATCTTGG	TTTTACATCA	AAGAAAATGG	360
AAACTATGCT	GATAAAGAAT	GGATTTTCGA	GAATGGTCAC	TATTATTATC	TAAAATCCGG	420
TGGCTACATG	GCAGCCAATG	AATGGATTTG	GGATAAGGAA	TCTTGGTTTT	ATCTCAAATT	480
TGATGGGAAA	ATGGCTGAAA	AAGAATGGGT	CTACGATTCT	CATAGTCAAG	CTTGGTACTA	540
CTTCAAATCC	GGTGGTTACA	TGACAGCCAA	TGAATGGATT	TGGGATAAGG	AATCTTGGTT	600
TTATCTCAAA	TCTGATGGGA	AAATAGCTGA	AAAAGAATGG	GTCTACGATT	CTCATAGTCA	660
AGCTTGGTAC	TACTTCAAAT	CCGGTGGTTA	CATGACAGCC	AATGAATGGA	TTTGGGATAA	720
GGAATCTTGG	TTTTACCTCA	AATCTGATGG	GAAAATAGCT	GAAAAAGAAT	GGGTC TACGA	780
TTCTCATAGT	CAAGCTTGGT	ACTACTTCAA	ATCTGGTGGC	TACATGGCGA	AAAATGAGAC	840
AGTAGATGGT	TATCAGCTTG	GAAGCGATGG	TAAATGGCTT	GGAGGAAAAA	CTACAAATGA	900
AAATGCTGCT	TACTATCAAG	TAGTGCCTGT	TACAGCCAAT	GTTTATGATT	CAGATGGTGA	960
AAAGCTTTCC	TATATATCGC	AAGGTAGTGT	CGTATGGCTA	GATAAGGATA	GAAAAAGTGA	1020
TGACAAGCGC	TTGGCTATTA	CTATTTCTGG	TTTGTCAGGC	TATATGAAAA	CAGAAGATTT	1080
ACAAGCGCTA	GATGCTAGTA	AGGACTTTAT	CCCTTATTAT	GAGAGTGATG	GCCACCGTTT	1140
TTATCACTAT	GTGGCTCAGA	ATGCTAGTAT	CCCAGTAGCT	TCTCATCTTT	CTGATATGGA	1200
AGTAGGCAAG	AAATATTATT	CGGCAGATGG	CCTGCATTTT	GATGGTTTTA	AGCTTGAGAA	1260
TCCCTTCCTT	TTCAAAGATT	TAACAGAGGC	TACAAACTAC	AGTGCTGAAG	AATTGGATAA	1320
GGTATTTAGT	TTGCTAAACA	TTAACAATAG	CCTTTTGGAG	AACAAGGGCG	CTACTTTTAA	1380
GGAAGCCGAA	GAACATTACC	ATATCAATGC	TCTTTATCTC	CTTGCCCATTA	GTGCCCTAGA	1440
AAGTAACTGG	GGAAGAAGTA	AAATTGCCAA	AGATAAGAAT	AATTTCTTTG	GCATTACAGC	1500
CTATGATACG	ACCCCTTACC	TTTCTGCTAA	GACATTTGAT	GATGTGGATA	AGGGAATTTT	1560
AGGTGCAACC	AAGTGGATTA	AGGAAAATTA	TATCGATAGG	GGAAGAACTT	TCCTTGGAAT	1620
CAAGGCTTCT	GGTATGAATG	TGGAATATGC	TTCAGACCCCT	TATTGGGGCG	AAAAAATTGC	1680

TAGTGTGATG ATGAAAATCA ATGAGAAG

1708


## (2) INFORMATION FOR SEQ ID NO:154:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:



Ala Lys Ser Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp  
 1 5 10 15  
 Gln Asp Gly Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val  
 20 25 30  
 Gly Ala Thr Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln  
 35 40 45  
 Tyr Asp Ala Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys  
 50 55 60  
 Glu Trp Leu Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly  
 65 70 75 80  
 Tyr Leu Leu Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser  
 85 90 95  
 Gly Ala Lys Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser  
 100 105 110  
 Trp Phe Tyr Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile  
 115 120 125  
 Phe Glu Asn Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala  
 130 135 140  
 Ala Asn Glu Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe  
 145 150 155 160  
 Asp Gly Lys Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln  
 165 170 175  
 Ala Trp Tyr Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp  
 180 185 190  
 Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile  
 195 200 205  
 Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr  
 210 215 220  
 Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp Lys  
 225 230 235 240  
 Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys Glu  
 245 250 255  
 Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser Gly

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 946 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ATTTGCAGAT GATTCTGAAG GATGGCAGTT TGTCCAAGAA AATGGTAGAA CCTACTACAA 60  
AAAGGGGGAT CTAAGAGAAA CCTACTGGAG AGTGATAGAT GGGAAGTACT ATTATTTTGA 120  
TCCTTTATCC GGAGAGATGG TTGTCGGCTG GCAATATATA CCTGCTCCAC ACAAGGGGGT 180  
TACGATTGGT CCTTCTCCAA GAATAGAGAT TGCTCTTAGA CCAGATTGGT TTTATTTTGG 240  
TCAAGATGGT GTATTACAAG AATTTGTTGG CAAGCAAGTT TTAGAAGCAA AAAC TGCTAC 300  
GAATACCAAC AAACATCATG GGGAAGAATA TGATAGCCAA GCAGAGAAAC GAGTCTATTA 360  
TTTTGAAGAT CAGCGTAGTT ATCATACTTT AAAA ACTGGT TGGATTTATG AAGAGGGTCA 420  
TTGGTATTAT TTACAGAAGG ATGGTGGCTT TGATTCGCGC ATCAACAGAT TGACGGTTGG 480  
AGAGCTAGCA CGTGGTTGGG TTAAGGATTA CCCTCTTACG TATGATGAAG AGAAGCTAAA 540  
AGCAGCTCCA TGGTACTATC TAAATCCAGC AACTGGCATT ATGCAAACAG GTTGGCAATA 600  
TCTAGGTAAT AGATGGTACT ACCTCCATTC GTCAGGAGCT ATGGCAACTG GCTGGTATAA 660  
GGAAGGCTCA ACTTGGTACT ATCTAGATGC TGAAAATGGT GATATGAGAA CTGGCTGGCA 720  
AAACCTTGGG AACAAATGGT ACTATCTCCG TTCATCAGGA GCTATGGCAA CTGGTTGGTA 780  
TCAGGAAAGT TCGACTTGGT ACTATCTAAA TGCAAGTAAT GGAGATATGA AAACAGGCTG 840  
GTTCCAAGTC AATGGTAACT GGTACTATGC CTATGATTCA GGTGCTTTAG CTGTTAATAC 900  
CACAGTAGGT GGT TACTACT TAAACTATAA TGGTGAATGG GTTAAG 946

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 316 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Val	Phe	Ala	Asp	Asp	Ser	Glu	Gly	Trp	Gln	Phe	Val	Gln	Glu	Asn	Gly
1				5				10						15	
Arg	Thr	Tyr	Tyr	Lys	Lys	Gly	Asp	Leu	Lys	Glu	Thr	Tyr	Trp	Arg	Val
			20				25						30		
Ile	Asp	Gly	Lys	Tyr	Tyr	Tyr	Phe	Asp	Pro	Leu	Ser	Gly	Glu	Met	Val
		35					40					45			
Val	Gly	Trp	Gln	Tyr	Ile	Pro	Ala	Pro	His	Lys	Gly	Val	Thr	Ile	Gly
	50					55					60				

Pro Ser Pro Arg Ile Glu Ile Ala Leu Arg Pro Asp Trp Phe Tyr Phe  
 65 70 75 80  
 Gly Gln Asp Gly Val Leu Gln Glu Phe Val Gly Lys Gln Val Leu Glu  
 85 90 95  
 Ala Lys Thr Ala Thr Asn Thr Asn Lys His His Gly Glu Glu Tyr Asp  
 100 105 110  
 Ser Gln Ala Glu Lys Arg Val Tyr Tyr Phe Glu Asp Gln Arg Ser Tyr  
 115 120 125  
 His Thr Leu Lys Thr Gly Trp Ile Tyr Glu Glu Gly His Trp Tyr Tyr  
 130 135 140  
 Leu Gln Lys Asp Gly Gly Phe Asp Ser Arg Ile Asn Arg Leu Thr Val  
 145 150 155 160  
 Gly Glu Leu Ala Arg Gly Trp Val Lys Asp Tyr Pro Leu Thr Tyr Asp  
 165 170 175  
 Glu Glu Lys Leu Lys Ala Ala Pro Trp Tyr Tyr Leu Asn Pro Ala Thr  
 180 185 190  
 Gly Ile Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Arg Trp Tyr Tyr  
 195 200 205  
 Leu His Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Lys Glu Gly Ser  
 210 215 220  
 Thr Trp Tyr Tyr Leu Asp Ala Glu Asn Gly Asp Met Arg Thr Gly Trp  
 225 230 235 240  
 Gln Asn Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met  
 245 250 255  
 Ala Thr Gly Trp Tyr Gln Glu Ser Ser Thr Trp Tyr Tyr Leu Asn Ala  
 260 265 270  
 Ser Asn Gly Asp Met Lys Thr Gly Trp Phe Gln Val Asn Gly Asn Trp  
 275 280 285  
 Tyr Tyr Ala Tyr Asp Ser Gly Ala Leu Ala Val Asn Thr Thr Val Gly  
 290 295 300  
 Gly Tyr Tyr Leu Asn Tyr Asn Gly Glu Trp Val Lys  
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

TGTCGCTGCA AATGAAACTG AAGTAGCAAA AACTTCGCAG GATACAACGA CAGCTTCAAG 60  
 TAGTTCAGAG CAAAATCAGT CTTCTAATAA AACGCAAACG AGCGCAGAAG TACAGACTAA 120

TGCTGCTGCC CACTGGGATG GGGATTATTA TGTAAGGAT GATGGTTCTA AAGCTCAAAG 180  
 TGAATGGATT TTTGACAACT ACTATAAGGC TTGGTTTTAT ATTAATTCAG ATGGTCGTTA 240  
 CTCGCAGAAT GAATGGCATG GAAATTACTA CCTGAAATCA GGTGGATATA TGGCCCAAAA 300  
 CGAGTGGATC TATGACAGTA ATTACAAGAG TTGGTTTTAT CTCAAGTCAG ATGGGGCTTA 360  
 TGCTCATCAA GAATGGCAAT TGATTGGAAA TAAGTGGTAC TACTTCAAGA AGTGGGGTTA 420  
 CATGGCTAAA AGCCAATGGC AAGGAAGTTA TTTCTTGAAT GGTCAAGGAG CTATGATGCA 480  
 AAATGAATGG CTSCATATGAT CCAGCCTATT CTGCTTATTT TTATCTAAAA TCCGATGGAA 540  
 CTTATGCTAA CCAAGAGTGG CAAAAAGTGG GCGGCAAATG GTACTATTTT AAGAAGTGGG 600  
 GCTATATGGC TCGGAATGAG TGGCAAGGCA ACTACTATTT GACTGGAAGT GGTGCCATGG 660  
 CGACTGACGA AGTGATTATG GATGGTACTC GCTATATCTT TCGGGCTCT GGTGAGCTCA 720  
 AAGAAAAAAA AGATTTGAAT GTCGGCTGGG TTCACAGAGA TGGTAAGCGC TATTTCTTTA 780  
 ATAATAGAGA AGAACAAGTG GGAACCGAAC ATGCTAAGAA AGTCATTGAT ATTAGTGAGC 840  
 ACAATGGTCG TATCAATGAT TGGAAAAAGG TTATTGATGA GAACGAAGTG GATGGTGTCA 900  
 TTGTTTCGTCT AGGTTATAGC GGTAAAGAAG ACAAGGAATT GCGGCATAAC ATTAAGGAGT 960  
 TAAACCGTCT GGGAATTCCT TATGGTGTCT ATCTCTATAC CTATGCTGAA AATGAGACCG 1020  
 ATGCTGAGAG TGACGCTAAA CAGACCATTG AACTTATAAA GAAATACAAT ATGAACCTGT 1080  
 CTTACCCTAT CTATTATGAT GTTGAGAATT GGAATATGT AAATAAGAGC AAGAGAGCTC 1140  
 CAAGTGATAC AGGCACCTGG GTTAAAATCA TCAACAAGTA CATGGACACG ATGAAGCAGG 1200  
 CGGGTTATCA AAATGTGTAT GTCTATAGCT ATCGTAGTTT ATTACAGACG CGTTTAAAC 1260  
 ACCCAGATAT TTTAAACAT GTAACTGGG TAGCGGCCTA TACGAATGCT TTAGAATGGG 1320  
 AAAACCTCA TTATTCAGGA AAAAAAGGTT GGCAATATAC CTCTTCTGAA TACATGAAAG 1380  
 GAATCCAAGG GCGCGTAGAT GTCAGCGTTT GGTAT 1415

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Val Ala Ala Asn Glu Thr Glu Val Ala Lys Thr Ser Gln Asp Thr Thr  
 1 5 10  
 Thr Ala Ser Ser Ser Ser Glu Gln Asn Gln Ser Ser Asn Lys Thr Gln  
 20 25 30  
 Thr Ser Ala Glu Val Gln Thr Asn Ala Ala Ala His Trp Asp Gly Asp

35					40					45					
Tyr	Tyr	Val	Lys	Asp	Asp	Gly	Ser	Lys	Ala	Gln	Ser	Glu	Trp	Ile	Phe
50						55					60				
Asp	Asn	Tyr	Tyr	Lys	Ala	Trp	Phe	Tyr	Ile	Asn	Ser	Asp	Gly	Arg	Tyr
65					70					75					80
Ser	Gln	Asn	Glu	Trp	His	Gly	Asn	Tyr	Tyr	Leu	Lys	Ser	Gly	Gly	Tyr
			85						90					95	
Met	Ala	Gln	Asn	Glu	Trp	Ile	Tyr	Asp	Ser	Asn	Tyr	Lys	Ser	Trp	Phe
			100					105					110		
Tyr	Leu	Lys	Ser	Asp	Gly	Ala	Tyr	Ala	His	Gln	Glu	Trp	Gln	Leu	Ile
		115					120					125			
Gly	Asn	Lys	Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Lys	Ser
	130					135					140				
Gln	Trp	Gln	Gly	Ser	Tyr	Phe	Leu	Asn	Gly	Gln	Gly	Ala	Met	Met	Gln
145					150					155					160
Asn	Glu	Trp	Leu	Tyr	Asp	Pro	Ala	Tyr	Ser	Ala	Tyr	Phe	Tyr	Leu	Lys
				165					170					175	
Ser	Asp	Gly	Thr	Tyr	Ala	Asn	Gln	Glu	Trp	Gln	Lys	Val	Gly	Gly	Lys
			180					185					190		
Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Arg	Asn	Glu	Trp	Gln
		195					200					205			
Gly	Asn	Tyr	Tyr	Leu	Thr	Gly	Ser	Gly	Ala	Met	Ala	Thr	Asp	Glu	Val
	210					215					220				
Ile	Met	Asp	Gly	Thr	Arg	Tyr	Ile	Phe	Ala	Ala	Ser	Gly	Glu	Leu	Lys
225					230					235					240
Glu	Lys	Lys	Asp	Leu	Asn	Val	Gly	Trp	Val	His	Arg	Asp	Gly	Lys	Arg
				245					250					255	
Tyr	Phe	Phe	Asn	Asn	Arg	Glu	Glu	Gln	Val	Gly	Thr	Glu	His	Ala	Lys
			260					265					270		
Lys	Val	Ile	Asp	Ile	Ser	Glu	His	Asn	Gly	Arg	Ile	Asn	Asp	Trp	Lys
		275					280					285			
Lys	Val	Ile	Asp	Glu	Asn	Glu	Val	Asp	Gly	Val	Ile	Val	Arg	Leu	Gly
		290				295					300				
Tyr	Ser	Gly	Lys	Glu	Asp	Lys	Glu	Leu	Ala	His	Asn	Ile	Lys	Glu	Leu
305					310					315					320
Asn	Arg	Leu	Gly	Ile	Pro	Tyr	Gly	Val	Tyr	Leu	Tyr	Thr	Tyr	Ala	Glu
				325					330					335	
Asn	Glu	Thr	Asp	Ala	Glu	Ser	Asp	Ala	Lys	Gln	Thr	Ile	Glu	Leu	Ile
			340					345					350		
Lys	Lys	Tyr	Asn	Met	Asn	Leu	Ser	Tyr	Pro	Ile	Tyr	Tyr	Asp	Val	Glu
		355					360					365			
Asn	Trp	Glu	Tyr	Val	Asn	Lys	Ser	Lys	Arg	Ala	Pro	Ser	Asp	Thr	Gly
	370					375					380				

Thr Trp Val Lys Ile Ile Asn Lys Tyr Met Asp Thr Met Lys Gln Ala  
 385 390 395 400  
 Gly Tyr Gln Asn Val Tyr Val Tyr Ser Tyr Arg Ser Leu Leu Gln Thr  
 405 410 415  
 Arg Leu Lys His Pro Asp Ile Leu Lys His Val Asn Trp Val Ala Ala  
 420 425 430  
 Tyr Thr Asn Ala Leu Glu Trp Glu Asn Pro His Tyr Ser Gly Lys Lys  
 435 440 445  
 Gly Trp Gln Tyr Thr Ser Ser Glu Tyr Met Lys Gly Ile Gln Gly Arg  
 450 455 460  
 Val Asp Val Ser Val Trp Tyr  
 465 470

## (2) INFORMATION FOR SEQ ID NO: 159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1924 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

TACGTCTCAG CCTACTTTTG TAAGAGCAGA AGAATCTCCA CAAGTTGTCG AAAAATCTTC 60  
 ATTAGAGAAG AAATATGAGG AAGCAAAAGC AAAAGCTGAT ACTGCCAAGA AAGATTACGA 120  
 AACGGCTAAA AAGAAAGCAG AAGACGCTCA GAAAAAGTAT GAAGATGATC AGAAGAGAAC 180  
 TGAGGAGAAA GCTCGAAAAG AAGCAGAAGC ATCTCAAAAA TTGAATGATG TGGCGCTTGT 240  
 TGTTCAAAAT GCATATAAAG AGTACCGAGA AGTTCAAAAT CAACGTAGTA AATATAAATC 300  
 TGACGCTGAA TATCAGAAAA AATTAACAGA GGTCGACTCT AAAATAGAGA AGGCTAGGAA 360  
 AGAGCAACAG GACTTGCAAA ATAAATTTAA TGAAGTAAGA GCAGTTGTAG TTCCTGAACC 420  
 AAATGCGTTG GCTGAGACTA AGAAAAAGC AGAAGAAGCT AAAGCAGAAG AAAAAGTAGC 480  
 TAAGAGAAAA TATGATTATG CAACTCTAAA GGTAGCATA GCGAAGAAAG AAGTAGAGGC 540  
 TAAGGAACTT GAAATTGAAA AACTTCAATA TGAAATTTCT ACTTTGGAAC AAGAAGTTGC 600  
 TACTGCTCAA CATCAAGTAG ATAATTTGAA AAAACTTCTT GCTGGTGCGG ATCCTGATGA 660  
 TGGCACAGAA GTTATAGAAG CTAAATTAAA AAAAGGAGAA GCTGAGCTAA ACGCTAAACA 720  
 AGCTGAGTTA GCAAAAAAAC AAACAGAACT TGAAAACTT CTTGACAGCC TTGATCCTGA 780  
 AGGTAAGACT CAGGATGAAT TAGATAAAGA AGCAGAAGAA GCTGAGTTGG ATAAAAAGC 840  
 TGATGAACTT CAAAATAAAG TTGCTGATTT AGAAAAAGAA ATTAGTAACC TTGAAATATT 900  
 ACTTGGAGGG GCTGATNCTG AAGATGATAC TGCTGCTCTT CAAAATAAAT TAGCTACTAA 960  
 AAAAGCTGAA TTGGAAAAAA CTCAAAAAGA ATTAGATGCA GCTCTTAATG AGTTAGGCCC 1020



TGATGGAGAT GAAGAAGAAA CTCCAGCGCC GGCTCCTCAA CCAGAGCAAC CAGCTCCTGC 1080  
 ACCAAAACCA GAGCAACCAG CTCCAGCTCC AAAACCAGAG CAACCAGCTC CTGCACCAAA 1140  
 ACCAGAGCAA CCAGCTCCAG CTCCAAAACC AGAGCAACCA GCTCCAGCTC CAAAACCAGA 1200  
 GCAACCAGCT AAGCCGGAGA AACCAGCTGA AGAGCCTACT CAACCAGAAA AACCAGCCAC 1260  
 TCCAAAAACA GGCTGGAAAC AAGAAAACGG TATGTGGTAT TTCTACAATA CTGATGGTTC 1320  
 AATGGCAATA GGTGGCTCC AAAACAACGG TTCATGGTAC TACCTAAACG CTAACGGCGC 1380  
 TATGGCAACA GGTGGGTGA AAGATGGAGA TACCTGGTAC TATCTTGAAG CATCAGGTGC 1440  
 TATGAAAGCA AGCCAATGGT TCAAAGTATC AGATAAATGG TACTATGTCA ACAGCAATGG 1500  
 CGCTATGGCG ACAGGCTGGC TCCAATACAA TGGCTCATGG TACTACCTCA ACGCTAATGG 1560  
 TGATATGGCG ACAGGATGGC TCCAATACAA CGGTTCATGG TATTACCTCA ACGCTAATGG 1620  
 TGATATGGCG ACAGGATGGG CTAAAGTCAA CGGTTCATGG TACTACCTAA ACGCTAACGG 1680  
 TGCTATGGCT ACAGGTTGGG CTAAAGTCAA CGGTTCATGG TACTACCTAA ACGCTAACGG 1740  
 TTCAATGGCA ACAGGTTGGG TGAAAGATGG AGATACCTGG TACTATCTTG AAGCATCAGG 1800  
 TGCTATGAAA GCAAGCCAAT GGTTCAAAGT ATCAGATAAA TGGTACTATG TCAATGGCTT 1860  
 AGGTGCCCTT GCAGTCAACA CAACTGTAGA TGGCTATAAA GTCAATGCCA ATGGTGAATG 1920  
 GGT 1924

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Thr	Ser	Gln	Pro	Thr	Phe	Val	Arg	Ala	Glu	Glu	Ser	Pro	Gln	Val	Val
1				5					10					15	
Glu	Lys	Ser	Ser	Leu	Glu	Lys	Lys	Tyr	Glu	Glu	Ala	Lys	Ala	Lys	Ala
			20					25					30		
Asp	Thr	Ala	Lys	Lys	Asp	Tyr	Glu	Thr	Ala	Lys	Lys	Lys	Ala	Glu	Asp
		35					40					45			
Ala	Gln	Lys	Lys	Tyr	Glu	Asp	Asp	Gln	Lys	Arg	Thr	Glu	Glu	Lys	Ala
		50				55					60				
Arg	Lys	Glu	Ala	Glu	Ala	Ser	Gln	Lys	Leu	Asn	Asp	Val	Ala	Leu	Val
65				70					75					80	
Val	Gln	Asn	Ala	Tyr	Lys	Glu	Tyr	Arg	Glu	Val	Gln	Asn	Gln	Arg	Ser
			85					90						95	

Lys Tyr Lys Ser Asp Ala Glu Tyr Gln Lys Lys Leu Thr Glu Val Asp  
 100 105 110  
 Ser Lys Ile Glu Lys Ala Arg Lys Glu Gln Gln Asp Leu Gln Asn Lys  
 115 120 125  
 Phe Asn Glu Val Arg Ala Val Val Val Pro Glu Pro Asn Ala Leu Ala  
 130 135 140  
 Glu Thr Lys Lys Lys Ala Glu Glu Ala Lys Ala Glu Glu Lys Val Ala  
 145 150 155 160  
 Lys Arg Lys Tyr Asp Tyr Ala Thr Leu Lys Val Ala Leu Ala Lys Lys  
 165 170 175  
 Glu Val Glu Ala Lys Glu Leu Glu Ile Glu Lys Leu Gln Tyr Glu Ile  
 180 185 190  
 Ser Thr Leu Glu Gln Glu Val Ala Thr Ala Gln His Gln Val Asp Asn  
 195 200 205  
 Leu Lys Lys Leu Leu Ala Gly Ala Asp Pro Asp Asp Gly Thr Glu Val  
 210 215 220  
 Ile Glu Ala Lys Leu Lys Lys Gly Glu Ala Glu Leu Asn Ala Lys Gln  
 225 230 235 240  
 Ala Glu Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys Leu Leu Asp Ser  
 245 250 255  
 Leu Asp Pro Glu Gly Lys Thr Gln Asp Glu Leu Asp Lys Glu Ala Glu  
 260 265 270  
 Glu Ala Glu Leu Asp Lys Lys Ala Asp Glu Leu Gln Asn Lys Val Ala  
 275 280 285  
 Asp Leu Glu Lys Glu Ile Ser Asn Leu Glu Ile Leu Leu Gly Gly Ala  
 290 295 300  
 Asp Xaa Glu Asp Asp Thr Ala Ala Leu Gln Asn Lys Leu Ala Thr Lys  
 305 310 315 320  
 Lys Ala Glu Leu Glu Lys Thr Gln Lys Glu Leu Asp Ala Ala Leu Asn  
 325 330 335  
 Glu Leu Gly Pro Asp Gly Asp Glu Glu Glu Thr Pro Ala Pro Ala Pro  
 340 345 350  
 Gln Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro  
 355 360 365  
 Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro  
 370 375 380  
 Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu  
 385 390 395 400  
 Gln Pro Ala Lys Pro Glu Lys Pro Ala Glu Glu Pro Thr Gln Pro Glu  
 405 410 415  
 Lys Pro Ala Thr Pro Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp  
 420 425 430  
 Tyr Phe Tyr Asn Thr Asp Gly Ser Met Ala Ile Gly Trp Leu Gln Asn

435                      440                      445  
 Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly  
 450                      455                      460  
 Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala  
 465                      470                      475                      480  
 Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val  
 485                      490                      495  
 Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser  
 500                      505                      510  
 Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Leu Gln  
 515                      520                      525  
 Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr  
 530                      535                      540  
 Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly  
 545                      550                      555                      560  
 Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu  
 565                      570                      575  
 Asn Ala Asn Gly Ser Met Ala Thr Gly Trp Val Lys Asp Gly Asp Thr  
 580                      585                      590  
 Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser Gln Trp Phe  
 595                      600                      605  
 Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala  
 610                      615                      620  
 Val Asn Thr Thr Val Asp Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp  
 625                      630                      635                      640  
 Val

## (2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 670 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

TGGACAGGTG AAAGGTCATG CTACATTTGT GAAATCCATG ACAACTGAAA TGTACCAAGA	60
ACAACAGAAC CATTCCTCTCG CCTACAATCA ACGCTTGGNT TCGCAAAATC GCATTGTAGA	120
TCCTTTTTTTG GCGGAGGGAT ATGAGGTCAA TTACCAAGTG TCTGACGACC CTGATGCAGT	180
CTATGGTTAC TTGTCTATTC CAAGTTTGGG AATCATGGAG CCGGTTTATT TGGGAGCAGA	240
TTATCATCAT TTAGGGATGG GCTTGGCTCA TGTGGATGGT ACACCGCTGC CTCTGGATGG	300
TACAGGGATT CGCTCAGTGA TTGCTGGGCA CCGTGCAGAG CCAAGCCATG TCTTTTCCG	360

CCATTTGGAT CAGCTAAAAG TTGGAGATGC TCTTTATTAT GATAATGGCC AGGAAATTGT 420  
 AGAATATCAG ATGATGGACA CAGAGATTAT TTTACCGTCG GAATGGGAAA AATTAGAATC 480  
 GGTTAGCTCT AAAAATATCA TGACCTTGAT AACCTGCGAT CCGATTCCCTA CCTTTAATAA 540  
 ACGCTTATTA GTGAATTTTG AACGAGTCGC TGT'TTATCAA AAATCAGATC CACAAACAGC 600  
 TGCAGTTGCG AGGGTTGCTT TTACGAAAGA AGGACAATCT GTATCGCGTG TTGCAACCTC 660  
 TCAATGGTTG 670

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Gly Gln Val Lys Gly His Ala Thr Phe Val Lys Ser Met Thr Thr Glu  
 1 5 10 15  
 Met Tyr Gln Glu Gln Gln Asn His Ser Leu Ala Tyr Asn Gln Arg Leu  
 20 25 30  
 Xaa Ser Gln Asn Arg Ile Val Asp Pro Phe Leu Ala Glu Gly Tyr Glu  
 35 40 45  
 Val Asn Tyr Gln Val Ser Asp Asp Pro Asp Ala Val Tyr Gly Tyr Leu  
 50 55 60  
 Ser Ile Pro Ser Leu Glu Ile Met Glu Pro Val Tyr Leu Gly Ala Asp  
 65 70 75 80  
 Tyr His His Leu Gly Met Gly Leu Ala His Val Asp Gly Thr Pro Leu  
 85 90 95  
 Pro Leu Asp Gly Thr Gly Ile Arg Ser Val Ile Ala Gly His Arg Ala  
 100 105 110  
 Glu Pro Ser His Val Phe Phe Arg His Leu Asp Gln Leu Lys Val Gly  
 115 120 125  
 Asp Ala Leu Tyr Tyr Asp Asn Gly Gln Glu Ile Val Glu Tyr Gln Met  
 130 135 140  
 Met Asp Thr Glu Ile Ile Leu Pro Ser Glu Trp Glu Lys Leu Glu Ser  
 145 150 155 160  
 Val Ser Ser Lys Asn Ile Met Thr Leu Ile Thr Cys Asp Pro Ile Pro  
 165 170 175  
 Thr Phe Asn Lys Arg Leu Leu Val Asn Phe Glu Arg Val Ala Val Tyr  
 180 185 190  
 Gln Lys Ser Asp Pro Gln Thr Ala Ala Val Ala Arg Val Ala Phe Thr  
 195 200 205

Lys Glu Gly Gln Ser Val Ser Arg Val Ala Thr Ser Gln Trp Leu  
 210 215 220

## (2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 784 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

GATTGCTCCT TTGAAGGATT TGAGAGAAAC CATGTTGGAA ATTGCTTCTG GTGCTCAAAA 60  
 TCTTCGTGCC AAGGAAGTTG GTGCCTATGA ACTGAGAGAA GTAACCTCGCC AATTTAATGC 120  
 TATGTTGGAT CAGATTGATC AGTTGATGGT AGCTATTCGT AGCCAGGAAG AAACGACCCG 180  
 TCAGTACCAA CTTCAAGCCC TTTGAGGCCA GATTAATCCA CATTTCTCTCT ATAACACTTT 240  
 GGACACCATC ATCTGGATGG CTGAATTTCA TGATAGTCAG CGAGTGGTGC AGGTGACCAA 300  
 GTCCTTGGCA ACCTATTTCC GCTTGGCGCT CAATCAAGGC AAGGACTTGA TTTGTCTCTC 360  
 TGACGAAATC AATCATGTCC GCCAGTATCT CTTTATCCAG AAACAACGCT ATGGAGATAA 420  
 GCTGGAATAC GAAATTAATG AAAATGTTGC CTTTGATAAT TTAGTCTTAC CCAAGCTGGT 480  
 CCTACAACCC CTTGTAGAAA ATGCTCTTTA CCATGGCATT AAGGAAAAGG AAGGTCAGGG 540  
 CCATATTAAA CTTTCTGTCC AGAAACAGGA TTCGGGATTG GTCATCCGTA TTGAGGATGA 600  
 TGGCGTTGGC TTCCAAGATG CTGGTGATAG TAGTCAAAGT CAACTCAAAC GTGGGGGAGT 660  
 TGGTCTTCAA AATGTCGATC AACGGCTCAA ACTTCATTTT GGAGCCAATT ACCATATGAA 720  
 GATTGATTCT AGACCCCAAA AAGGGACGAA AGTTGAAATA TATATAAATA GAATAGAAAC 780  
 TAGC 784

## (2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 261 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ile Ala Pro Leu Lys Asp Leu Arg Glu Thr Met Leu Glu Ile Ala Ser  
 1 5 10 15  
 Gly Ala Gln Asn Leu Arg Ala Lys Glu Val Gly Ala Tyr Glu Leu Arg  
 20 25 30  
 Glu Val Thr Arg Gln Phe Asn Ala Met Leu Asp Gln Ile Asp Gln Leu

35                      40                      45  
 Met Val Ala Ile Arg Ser Gln Glu Glu Thr Thr Arg Gln Tyr Gln Leu  
   50                      55                      60  
 Gln Ala Leu Ser Ser Gln Ile Asn Pro His Phe Leu Tyr Asn Thr Leu  
   65                      70                      75                      80  
 Asp Thr Ile Ile Trp Met Ala Glu Phe His Asp Ser Gln Arg Val Val  
                     85                      90                      95  
 Gln Val Thr Lys Ser Leu Ala Thr Tyr Phe Arg Leu Ala Leu Asn Gln  
                     100                      105                      110  
 Gly Lys Asp Leu Ile Cys Leu Ser Asp Glu Ile Asn His Val Arg Gln  
                     115                      120                      125  
 Tyr Leu Phe Ile Gln Lys Gln Arg Tyr Gly Asp Lys Leu Glu Tyr Glu  
                     130                      135                      140  
 Ile Asn Glu Asn Val Ala Phe Asp Asn Leu Val Leu Pro Lys Leu Val  
   145                      150                      155                      160  
 Leu Gln Pro Leu Val Glu Asn Ala Leu Tyr His Gly Ile Lys Glu Lys  
                     165                      170                      175  
 Glu Gly Gln Gly His Ile Lys Leu Ser Val Gln Lys Gln Asp Ser Gly  
                     180                      185                      190  
 Leu Val Ile Arg Ile Glu Asp Asp Gly Val Gly Phe Gln Asp Ala Gly  
                     195                      200                      205  
 Asp Ser Ser Gln Ser Gln Leu Lys Arg Gly Gly Val Gly Leu Gln Asn  
   210                      215                      220  
 Val Asp Gln Arg Leu Lys Leu His Phe Gly Ala Asn Tyr His Met Lys  
   225                      230                      235                      240  
 Ile Asp Ser Arg Pro Gln Lys Gly Thr Lys Val Glu Ile Tyr Ile Asn  
                     245                      250                      255  
 Arg Ile Glu Thr Ser  
                     260

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGGCTC CATAATATCT ATAAGGGATT	60
TACCCACTAC AAATATTATA GAGCCGAAAA TTCACATCTA ATATATGCAG ACTACTTTGA	120
AATGAAATTA AAAAAATTAT TAAAGGATGA CACAAAAGTT TTTGAAAAAT CTACATTCAA	180
ATTTGTAGAA GGATATAAAA TATACCTGAC AGAATCTAAA GAATCTGGAA TTAAACAAAT	240

GGACAATGTC ATAAAAATATT TTGAGTTTAT TGAATCTAAA AGTATTGCTT TATATTTTCA 300  
 AAAACGATTA AATGAGCTGA TAGAT 325

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Arg Ser Tyr Gly Thr Phe Phe Leu Gln Gln Asn Arg Leu His Asn Ile  
 1 5 10 15  
 Tyr Lys Gly Phe Thr His Tyr Lys Tyr Tyr Arg Ala Glu Asn Ser His  
 20 25 30  
 Leu Ile Tyr Ala Asp Tyr Phe Glu Met Lys Leu Lys Lys Leu Leu Lys  
 35 40 45  
 Asp Asp Thr Lys Val Phe Glu Lys Ser Thr Phe Lys Phe Val Glu Gly  
 50 55 60  
 Tyr Lys Ile Tyr Leu Thr Glu Ser Lys Glu Ser Gly Ile Lys Gln Met  
 65 70 75 80  
 Asp Asn Val Ile Lys Tyr Phe Glu Phe Ile Glu Ser Lys Ser Ile Ala  
 85 90 95  
 Leu Tyr Phe Gln Lys Arg Leu Asn Glu Leu Ile Asp  
 100 105

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 238 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CAACGTTGAG AATTATTTGC GAATGTGTTT GGATAGCATT CAGAATCAGA CGTATCAAAA 60  
 TTTTGAGTGT TTATTAATCA ATGATGGCTC TCCAGATCAT TCATCCAAAA TATGTGAAGA 120  
 ATTTGTAGAG AAAGATTCTC GTTTCAAATA TTTTGAGAAA GCAAACGGCG GTCTTTCATC 180  
 AGCTCGTAAC CTAGGTATTG AATGTTCCGGG GGGGGGCGTA CATTACTTTT GTAGACTC 238

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 79 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn	Val	Glu	Asn	Tyr	Leu	Arg	Met	Cys	Leu	Asp	Ser	Ile	Gln	Asn	Gln
1				5					10					15	
Thr	Tyr	Gln	Asn	Phe	Glu	Cys	Leu	Leu	Ile	Asn	Asp	Gly	Ser	Pro	Asp
			20					25					30		
His	Ser	Ser	Lys	Ile	Cys	Glu	Glu	Phe	Val	Glu	Lys	Asp	Ser	Arg	Phe
			35				40					45			
Lys	Tyr	Phe	Glu	Lys	Ala	Asn	Gly	Gly	Leu	Ser	Ser	Ala	Arg	Asn	Leu
	50					55					60				
Gly	Ile	Glu	Cys	Ser	Gly	Gly	Gly	Val	His	Tyr	Phe	Cys	Arg	Leu	
65					70				75						

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 742 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

CTACTATCAA TCAAGTTCCTT CAGCCATTGA GGCCACCATT GAGGGCAACA GCCAAACGAC	60
CATCAGCCAG ACTAGCCACT TTATTTCAGTC TTATATCAAA AACTAGAAA CCACCTCGAC	120
TGGTTTGACC CAGCAGACGG ATGTTCTGGC CTATGCTGAG AATCCCAGTC AAGACAAGGT	180
CGAGGGAATC CGAGATTTGT TTTTGACCAT CTTGAAGTCA GATAAGGACT TGAAAACGT	240
TGTGCTGGTG ACCAAATCTG GTCAGGTCAT TTCTACAGAT GACAGTGTGC AGATGAAAAC	300
TTCTCTGAT ATGATGGCTG AGGATTGGTA CAAAAGGCC ATTCATCAGG GAGCTATGCC	360
TGTTTTGACT CCAGCTCGTA AATCAGATAG TCAGTGGGTC ATTTCTGTCA CTCAAGAACT	420
TGTTGATGCA AAGGGAGCCA ATCTTGGTGT GCTTCGTTTG GATATTTCTT ATGAAACTCT	480
GGAAGCCTAT CTCAATCAAC TCCAGTTGGG GCAGCAGGGC TTTGCCTTCA TTATCAATGA	540
AAACCATGAA TTTGTCTACC ATCCTCAACA CACAGTTTAT AGTTCGTCTA GCAAAATGGA	600
GGCTATGAAA CCCTACATCG ATACAGGTCA GGGTTATACT CCTGGTCACA AATCCTACGT	660
CAGTCAAGAG AAGATTGCAG GAACTGATTG GACGGTGCTT GCGGTGTCAT CATTGGAAAA	720
GTTAGACCAG GTTCGGAGTC AG	742

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 247 amino acids



(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Tyr Tyr Gln Ser Ser Ser Ser Ala Ile Glu Ala Thr Ile Glu Gly Asn  
 1 5 10 15  
 Ser Gln Thr Thr Ile Ser Gln Thr Ser His Phe Ile Gln Ser Tyr Ile  
 20 25 30  
 Lys Lys Leu Glu Thr Thr Ser Thr Gly Leu Thr Gln Gln Thr Asp Val  
 35 40 45  
 Leu Ala Tyr Ala Glu Asn Pro Ser Gln Asp Lys Val Glu Gly Ile Arg  
 50 55 60  
 Asp Leu Phe Leu Thr Ile Leu Lys Ser Asp Lys Asp Leu Lys Thr Val  
 65 70 75 80  
 Val Leu Val Thr Lys Ser Gly Gln Val Ile Ser Thr Asp Asp Ser Val  
 85 90 95  
 Gln Met Lys Thr Ser Ser Asp Met Met Ala Glu Asp Trp Tyr Gln Lys  
 100 105 110  
 Ala Ile His Gln Gly Ala Met Pro Val Leu Thr Pro Ala Arg Lys Ser  
 115 120 125  
 Asp Ser Gln Trp Val Ile Ser Val Thr Gln Glu Leu Val Asp Ala Lys  
 130 135 140  
 Gly Ala Asn Leu Gly Val Leu Arg Leu Asp Ile Ser Tyr Glu Thr Leu  
 145 150 155 160  
 Glu Ala Tyr Leu Asn Gln Leu Gln Leu Gly Gln Gln Gly Phe Ala Phe  
 165 170 175  
 Ile Ile Asn Glu Asn His Glu Phe Val Tyr His Pro Gln His Thr Val  
 180 185 190  
 Tyr Ser Ser Ser Ser Lys Met Glu Ala Met Lys Pro Tyr Ile Asp Thr  
 195 200 205  
 Gly Gln Gly Tyr Thr Pro Gly His Lys Ser Tyr Val Ser Gln Glu Lys  
 210 215 220  
 Ile Ala Gly Thr Asp Trp Thr Val Leu Gly Val Ser Ser Leu Glu Lys  
 225 230 235 240  
 Leu Asp Gln Val Arg Ser Gln  
 245

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1282 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GACAAAAACA TTAAACGTC CTGAGGTTTT ATCACCTGCA GGGACTTTAG AGAAGCTAAA 60  
 GGTAGCTGTT CAGTATGGAG CAGATGCTGT CTTTATCGGT GGTCAGGCCT ATGGTCTTCG 120  
 TAGCCGTGCG GGAAACTTTA CTTTCGAACA GATGGAAGAA GCGGTGCAGT TTGCGGCCAA 180  
 GTATGGTGCC AAGGTCATATG TAGCGGCTAA TATGGTTATG CACGAAGGAA ATGAAGCTGG 240  
 TGCTGGTGAG TGGTTCGGTA AACTGCGTGA TATCGGGATT GCAGCAGTTA TCGTATCTGA 300  
 CCCAGCCTTG ATTATGATTG CAGTGACTGA AGCACCAGGC CTTGAAATCC ACCTTTCCTAC 360  
 CCAAGCCAGT GCCACTAACT ATGAAACCCT TGAGTCTCGG AAAGAGCTAG GCTTGACTCG 420  
 TGTCGTTTTA GCGCGTGAGG TTTCAATGGA AGAATTAGCT GAGATCCGCA AACGTACAGA 480  
 TGTGAAATT GAAGCCTTTG TCCATGGAGC TATGTGTATT TCATACTCTG GACGTTGTAC 540  
 TCTTTCAAAC CACATGAGTA TGCCTGATGC CAACCGTGGT GGATGTTCTC AGTCATGCCG 600  
 TTGGAATAC GACCTTTACG ATATGCCATT TGGGAAAGAA CGTAAGAGTT TGCAGGGTGA 660  
 GATTCCAGAA GAATTTTCAA TGTCAGCCGT TGACATGTCT ATGATTGACC ANATTCCAGA 720  
 TATGATTGAA AATGGTGTGG ACAGTCTAAA AATCGAAGGA CGTATGNAGT CTATTCACTA 780  
 NGTATCAACA GTAACCAACT GCTACAAGGC GGCTGTGGAT GCCTATCTTG AAAGTCCTGA 840  
 AAAGTTTGAA GCTATCAAAC AAGACTTGGT GGACGAGATG TGGAAGGTTG CCCAACGTGA 900  
 ACTGGCTACA GGATTTTACT ATGGTACACC ATCTGAAAAT GAGCAGTTGT TTGGTGCTCG 960  
 TCGTAAATC CCTGAGTACA AGTTTGTGCG TGAAGTGGTT TCTTATGATG ATGCGGCACA 1020  
 AACAGCAACT ATTCGTCAAC GAAACGTCAT TAACGAAGGG GACCAAGTTG AGTTTTATGG 1080  
 TCCAGGTTTC CGTCATTTTG AAACCTATAT TGAAGATTTG CATGATGCTA AAGGCAATAA 1140  
 AATCGACCGC GCTCCAAATC CAATGGAAC TTTGACTATT AAAGTCCCAC AACCTGTTCA 1200  
 ATCAGGAGAC ATGGTTCGAG CTCTTAAAGA GGGGCTTATC AATCTTTATA AGGAAGATGG 1260  
 AACCAGCGTC ACAGTTCGTG CT 1282

## (2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 427 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Thr Lys Thr Leu Lys Arg Pro Glu Val Leu Ser Pro Ala Gly Thr Leu  
 1 5 10 15

Glu Lys Leu Lys Val Ala Val Gln Tyr Gly Ala Asp Ala Val Phe Ile  
 20 25 30  
 Gly Gly Gln Ala Tyr Gly Leu Arg Ser Arg Ala Gly Asn Phe Thr Phe  
 35 40 45  
 Glu Gln Met Glu Glu Gly Val Gln Phe Ala Ala Lys Tyr Gly Ala Lys  
 50 55 60  
 Val Tyr Val Ala Ala Asn Met Val Met His Glu Gly Asn Glu Ala Gly  
 65 70 75 80  
 Ala Gly Glu Trp Phe Arg Lys Leu Arg Asp Ile Gly Ile Ala Ala Val  
 85 90 95  
 Ile Val Ser Asp Pro Ala Leu Ile Met Ile Ala Val Thr Glu Ala Pro  
 100 105 110  
 Gly Leu Glu Ile His Leu Ser Thr Gln Ala Ser Ala Thr Asn Tyr Glu  
 115 120 125  
 Thr Leu Glu Phe Trp Lys Glu Leu Gly Leu Thr Arg Val Val Leu Ala  
 130 135 140  
 Arg Glu Val Ser Met Glu Glu Leu Ala Glu Ile Arg Lys Arg Thr Asp  
 145 150 155 160  
 Val Glu Ile Glu Ala Phe Val His Gly Ala Met Cys Ile Ser Tyr Ser  
 165 170 175  
 Gly Arg Cys Thr Leu Ser Asn His Met Ser Met Arg Asp Ala Asn Arg  
 180 185 190  
 Gly Gly Cys Ser Gln Ser Cys Arg Trp Lys Tyr Asp Leu Tyr Asp Met  
 195 200 205  
 Pro Phe Gly Lys Glu Arg Lys Ser Leu Gln Gly Glu Ile Pro Glu Glu  
 210 215 220  
 Phe Ser Met Ser Ala Val Asp Met Ser Met Ile Asp Xaa Ile Pro Asp  
 225 230 235 240  
 Met Ile Glu Asn Gly Val Asp Ser Leu Lys Ile Glu Gly Arg Met Xaa  
 245 250 255  
 Ser Ile His Xaa Val Ser Thr Val Thr Asn Cys Tyr Lys Ala Ala Val  
 260 265 270  
 Asp Ala Tyr Leu Glu Ser Pro Glu Lys Phe Glu Ala Ile Lys Gln Asp  
 275 280 285  
 Leu Val Asp Glu Met Trp Lys Val Ala Gln Arg Glu Leu Ala Thr Gly  
 290 295 300  
 Phe Tyr Tyr Gly Thr Pro Ser Glu Asn Glu Gln Leu Phe Gly Ala Arg  
 305 310 315 320  
 Arg Lys Ile Pro Glu Tyr Lys Phe Val Ala Glu Val Val Ser Tyr Asp  
 325 330 335  
 Asp Ala Ala Gln Thr Ala Thr Ile Arg Gln Arg Asn Val Ile Asn Glu  
 340 345 350

Gly Asp Gln Val Glu Phe Tyr Gly Pro Gly Phe Arg His Phe Glu Thr  
 355 360 365  
 Tyr Ile Glu Asp Leu His Asp Ala Lys Gly Asn Lys Ile Asp Arg Ala  
 370 375 380  
 Pro Asn Pro Met Glu Leu Leu Thr Ile Lys Val Pro Gln Pro Val Gln  
 385 390 395 400  
 Ser Gly Asp Met Val Arg Ala Leu Lys Glu Gly Leu Ile Asn Leu Tyr  
 405 410 415  
 Lys Glu Asp Gly Thr Ser Val Thr Val Arg Ala  
 420 425

## (2) INFORMATION FOR SEQ ID NO: 173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

TTCTCAGGAG ACCTTTAAAA ATATCACCAA TAGCTTCTCC ATGCAAATCA ATCGTCGCGT 60  
 CAACCAAGGA ACGCCTCGTG GTGCTGGGAA TATCAAGGGT GAAGACATCA AAAAAATCAC 120  
 CGAAAACAAG GCCATTGAGT CTTATGTCAA ACGTATCAAC GCTATCGGAG ATTTGACTGG 180  
 ATATGACCTG ATTGAAACGC CAGAAACCAA GAAGAATCTC ACTGCTGATC GTGCCAAGCG 240  
 TTTTGGAAGT AGCTTGATGA TTACAGGTGT CAATGACTCC TCTAAAGAAG ACAAGTTTGT 300  
 CTCTGGTTCT TATAAACTAG TCGAAGGAGA GCACTTAACC AACGACGACA AGGATAAAAT 360  
 CCTCTTGACAC AAGGACTTGG CAGCCAAACA CGGCTGGAAA GTAGGGGACA AGGTTAAACT 420  
 GGACTCTAAT ATCTACGATG CAGATAATGA AAAAGGAGCC AAGGAAACAG TTGAAGTGAC 480  
 AATCAAGGGA CTCTTTGATG GTCATAATAA GTCAGCAGTA ACCTACTCAC AAGAACTTTA 540  
 CGAAAACACA GCTATTACAG ACATTACACAC TGCTGCAAAA CTTTATGGAT ACACAGAAGA 600  
 CACAGCCATT TATGGGGACG CAACCTTCTT TGTAACAGCA GACAAGAAGT TGGATGATGT 660  
 TATGAAAGAG TTGAATGGCA TCAGTGGTAT CAACTGGAAG AGCTACACAC TCGTCAAGAG 720  
 CTCCTCTAAC TACCCAGCTC TTGAGCAATC TATCTCTGGT ATGTACAAGA TGGCCAAC 778

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ser Gln Glu Thr Phe Lys Asn Ile Thr Asn Ser Phe Ser Met Gln Ile  
 1 5 10 15  
 Asn Arg Arg Val Asn Gln Gly Thr Pro Arg Gly Ala Gly Asn Ile Lys  
 20 25 30  
 Gly Glu Asp Ile Lys Lys Ile Thr Glu Asn Lys Ala Ile Glu Ser Tyr  
 35 40 45  
 Val Lys Arg Ile Asn Ala Ile Gly Asp Leu Thr Gly Tyr Asp Leu Ile  
 50 55 60  
 Glu Thr Pro Glu Thr Lys Lys Asn Leu Thr Ala Asp Arg Ala Lys Arg  
 65 70 75 80  
 Phe Gly Ser Ser Leu Met Ile Thr Gly Val Asn Asp Ser Ser Lys Glu  
 85 90 95  
 Asp Lys Phe Val Ser Gly Ser Tyr Lys Leu Val Glu Gly Glu His Leu  
 100 105 110  
 Thr Asn Asp Asp Lys Asp Lys Ile Leu Leu His Lys Asp Leu Ala Ala  
 115 120 125  
 Lys His Gly Trp Lys Val Gly Asp Lys Val Lys Leu Asp Ser Asn Ile  
 130 135 140  
 Tyr Asp Ala Asp Asn Glu Lys Gly Ala Lys Glu Thr Val Glu Val Thr  
 145 150 155 160  
 Ile Lys Gly Leu Phe Asp Gly His Asn Lys Ser Ala Val Thr Tyr Ser  
 165 170 175  
 Gln Glu Leu Tyr Glu Asn Thr Ala Ile Thr Asp Ile His Thr Ala Ala  
 180 185 190  
 Lys Leu Tyr Gly Tyr Thr Glu Asp Thr Ala Ile Tyr Gly Asp Ala Thr  
 195 200 205  
 Phe Phe Val Thr Ala Asp Lys Asn Leu Asp Asp Val Met Lys Glu Leu  
 210 215 220  
 Asn Gly Ile Ser Gly Ile Asn Trp Lys Ser Tyr Thr Leu Val Lys Ser  
 225 230 235 240  
 Ser Ser Asn Tyr Pro Ala Leu Glu Gln Ser Ile Ser Gly Met Tyr Lys  
 245 250 255  
 Met Ala Asn

## (2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 694 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

AGTAAATGCG CAATCAAATT CATTAATATT AATAGATGAA CCTGAAATCT CACTTCATCC 60  
 GAGTGCAATC TATAAATTTA AAGAGTTTTT ACTTCAAGAG TGTTTAAATA AAAAACATCA 120  
 AATTATTATC ACTACACATT CTACACAACCT TATAAAAGAT TTTCCCTAGAG AAGCCGTGAA 180  
 ACTTTTAGTG AAAAACGGAG AAAAGGTAGA TGTTATTGAA AATATTGATT ATCAGGATGC 240  
 ATTTTTTGAA TTAGGTGATG TGTATCATTC TAGGAAGATG ATTTATGTTG AAGATAGACT 300  
 AGCTAAATAT ATTCTAGAGT TTGTTATCAC TCATTCAAGT AGTGAGAATC TTAAACAGAA 360  
 TTTAGTAGTG AGATATATTC CTGGTGGAGC AAATCAAATA ATTTGTAATA ATATTTTAAA 420  
 CTCATCGTAT TTAGATTCCG ATAACCATTA TTTTGGCTT GATGGAGATC AAAACACTAA 480  
 TGTTAGTGAA TCAAATAATT TAATGAACCTA TCCTGAAAAT GGTGTTGTTA TATCAGATAA 540  
 AATTCCTGAA TCAGATAATA AAAATCTTGA TGATATTATA AAATTGATAA NGGGATGTCC 600  
 AATTAAATTT AATGTTTCAG GTAATAAAGG GCAAAAAAAT AATATTGAAT TAATTGCGAA 660  
 ACAAAGAAGC TTTATAGATT ATTGGGCTAA ATAC 694

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Val Asn Ala Gln Ser Asn Ser Leu Ile Leu Ile Asp Glu Pro Glu Ile  
 1 5 10 15  
 Ser Leu His Pro Ser Ala Ile Tyr Lys Phe Lys Glu Phe Leu Leu Gln  
 20 25 30  
 Glu Cys Leu Asn Lys Lys His Gln Ile Ile Ile Thr Thr His Ser Thr  
 35 40 45  
 Gln Leu Ile Lys Asp Phe Pro Arg Glu Ala Val Lys Leu Leu Val Lys  
 50 55 60  
 Asn Gly Glu Lys Val Asp Val Ile Glu Asn Ile Asp Tyr Gln Asp Ala  
 65 70 75 80  
 Phe Phe Glu Leu Gly Asp Val Tyr His Ser Arg Lys Met Ile Tyr Val  
 85 90 95  
 Glu Asp Arg Leu Ala Lys Tyr Ile Leu Glu Phe Val Ile Thr His Ser  
 100 105 110  
 Gly Ser Glu Asn Leu Lys Gln Asn Leu Val Val Arg Tyr Ile Pro Gly  
 115 120 125  
 Gly Ala Asn Gln Ile Ile Cys Asn Asn Ile Leu Asn Ser Ser Tyr Leu  
 130 135 140


Asp	Ser	Asp	Asn	His	Tyr	Phe	Trp	Leu	Asp	Gly	Asp	Gln	Asn	Thr	Asn
145					150					155					160
Val	Ser	Glu	Ser	Asn	Asn	Leu	Met	Asn	Tyr	Leu	Glu	Asn	Gly	Val	Val
				165					170					175	
Ile	Ser	Asp	Lys	Ile	Pro	Glu	Ser	Asp	Asn	Lys	Asn	Leu	Asp	Asp	Ile
			180					185					190		
Ile	Lys	Leu	Ile	Xaa	Gly	Cys	Pro	Ile	Lys	Phe	Asn	Val	Ser	Gly	Asn
		195					200					205			
Lys	Gly	Gln	Lys	Asn	Asn	Ile	Glu	Leu	Ile	Ala	Lys	Gln	Arg	Ser	Phe
	210					215					220				
Ile	Asp	Tyr	Trp	Ala	Lys	Tyr									
225					230										

## (2) INFORMATION FOR SEQ ID NO: 177:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:



TTACCGCGTT CATCAAGATG TCAAACAAGT CATGACCTAT CAACCCATGG TGCGAGAAAT	60
ATTGAGTGAA CAAGACACCC CAGCAAACGA AGAGCTTGTG CTTGCTATGA TTTATACTGA	120
AACAAAAGGA AAAGAAGGCG ATGTTATGCA GTCTAGTGAG TCTGCAAGTG GTTCCACCAA	180
CACCATCAAT GATAATGCCT CTAGCATTCG GCAAGGCATT CAAACTCTGA CAGGCAATCT	240
CTATCTGGCG CAGAAGAAGG GGGTAGATAT CTGGACAGCT GTTCAAGCCT ATAATTTTGG	300
ACCTGCCTAT ATCGATTTTA TCGCCCCAAA TGGCAAGGAA AATACCCTGG CTCTAGCCAA	360
ACAGTACTCT CGTGAGACTG TTGCCCCCTT GCTTGGTAAT AGGACTGGAA AGACTTATAG	420
TTATATTAC CCCATTTCCA TTTTTCACGG TGCTGAATC TATGTAAATG GAGGAAACTA	480
TTATTATTCT AGACAGGTAC GACTTAACCT TTACATCATC AAATGTTTCA CTCTCTTTTC	540
AACATCTGGC	550

## (2) INFORMATION FOR SEQ ID NO:178:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Tyr Arg Val His Gln Asp Val Lys Gln Val Met Thr Tyr Gln Pro Met  
 1 5 10 15  
 Val Arg Glu Ile Leu Ser Glu Gln Asp Thr Pro Ala Asn Glu Glu Leu  
 20 25 30  
 Val Leu Ala Met Ile Tyr Thr Glu Thr Lys Gly Lys Glu Gly Asp Val  
 35 40 45  
 Met Gln Ser Ser Glu Ser Ala Ser Gly Ser Thr Asn Thr Ile Asn Asp  
 50 55 60  
 Asn Ala Ser Ser Ile Arg Gln Gly Ile Gln Thr Leu Thr Gly Asn Leu  
 65 70 75 80  
 Tyr Leu Ala Gln Lys Lys Gly Val Asp Ile Trp Thr Ala Val Gln Ala  
 85 90 95  
 Tyr Asn Phe Gly Pro Ala Tyr Ile Asp Phe Ile Ala Gln Asn Gly Lys  
 100 105 110  
 Glu Asn Thr Leu Ala Leu Ala Lys Gln Tyr Ser Arg Glu Thr Val Ala  
 115 120 125  
 Pro Leu Leu Gly Asn Arg Thr Gly Lys Thr Tyr Ser Tyr Ile His Pro  
 130 135 140  
 Ile Ser Ile Phe His Gly Ala Glu Leu Tyr Val Asn Gly Gly Asn Tyr  
 145 150 155 160  
 Tyr Tyr Ser Arg Gln Val Arg Leu Asn Leu Tyr Ile Ile Lys Cys Phe  
 165 170 175  
 Thr Leu Phe Ser Thr Ser Gly  
 180

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GTGGATGGGC TTAACTATC TTCGTATTCG CCGTGC GGCT AAAATTGTGG ACAATGAGGA	60
GTTTGAAGCC TTGATTCGTA CGGGTCAATT GATTGATTG CGCGACCCAG CAGAATTCCA	120
CAGAAAACAT ATCCTTGGTG CACGCAATAT TCCTTCAAGT CAGTTGAAAA CTAGTCTTGC	180
AGCCCTTCGT AAAGATAAAC CTGTCCTTCT CTACGAAAAC CAACGTGCGC AACGAGTTAC	240
AAATGCAGCT CTTTACTTGA AAAACAAGG TTTTCTGAG ATTTATATCC TTTCTTATGG	300
CTTGGATTCT TGGAAAGGGA AAGTGAAGAC TAGC	334

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids



- (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Trp Met Gly Phe Asn Tyr Leu Arg Ile Arg Arg Ala Ala Lys Ile Val  
 1 5 10 15  
 Asp Asn Glu Glu Phe Glu Ala Leu Ile Arg Thr Gly Gln Leu Ile Asp  
 20 25 30  
 Leu Arg Asp Pro Ala Glu Phe His Arg Lys His Ile Leu Gly Ala Arg  
 35 40 45  
 Asn Ile Pro Ser Ser Gln Leu Lys Thr Ser Leu Ala Ala Leu Arg Lys  
 50 55 60  
 Asp Lys Pro Val Leu Leu Tyr Glu Asn Gln Arg Ala Gln Arg Val Thr  
 65 70 75 80  
 Asn Ala Ala Leu Tyr Leu Lys Lys Gln Gly Phe Ser Glu Ile Tyr Ile  
 85 90 95  
 Leu Ser Tyr Gly Leu Asp Ser Trp Lys Gly Lys Val Lys Thr Ser  
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 181:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ACTAAACCAG CATCGTTCGC AGGAAAATAA GGACAATAAT CGTGTCTCTT ATGTGGATGG 60  
 CAGCCAGTCA AGTCAGAAAA GTGAAAACCTT GACACCAGAC CAGGTTAGCC AGAAAGAAGG 120  
 AATTCAGGCT GAGCAAATTG TAATCAAAAT TACAGATCAG GGCTATGTAA CGTCACACGG 180  
 TGACCACTAT CATTACTATA ATGGGAAAGT TCCTTATGAT GCCCTCTTTA GTGAAGAACT 240  
 CTTGATGAAG GATCCAAACT ATCAACTTAA AGACGCTGAT ATTGTCAATG AAGTCAAGGG 300  
 TGGTTATATC ATCAAGGTCG ATGGAAAATA TTATGTCTAC CTGAAAGATG CAGCTCATGC 360  
 TGATAATGTT CGAACTAAAG ATGAAATCAA TCGTCAAAAA CAAGAACATG TCAAAGATAA 420  
 TGAGAAGGTT AACTCTAATG TTGCTGTAGC AAGGTCTCAG GGACGATATA CGACAAATGA 480  
 TGGTTATGTC TTTAATCCAG CTGATATTAT CGAAGATACG GGTAATGCTT ATATCGTTCC 540  
 TCATGGAGGT CACTATCACT ACATTCCCAA AAGCGATTTA TCTGCTAGTG AATTAGCAGC 600  
 AGCTAAAGCA CATCTGGCTG GAAAAAATAT GCAACCGAGT CAGTTAAGCT ATTCTTCAAC 660

AGCTAGTGAC AATAACACGC AATCTGTAGC AAAAGGATCA ACTAGCAAGC CAGCAAATAA 720  
 ATCTGAAAAT CTCCAGAGTC TTTTGAAGGA ACTCTATGAT TCACCTAGCG CCCAACGTTA 780  
 CAGTGAATCA GATGGCCTGG TCTTTGACCC TGCTAAGATT ATCAGTCGTA CACCAAATGG 840  
 AGTTGCGATT CCGCATGGCG ACCATTACCA CTTTATTCCT TACAGCAAGC TTTCTGCCTT 900  
 AGAAGAAAAG ATTGCCAGAA TGGTGCCTAT CAGTGGAAGT GGTTCCTACAG TTTCTACAAA 960  
 TGCAAAACCT AATGAAGTAG TGTCTAGTCT AGGCAGTCTT TCAAGCAATC CTTCTTCTTT 1020  
 AACGACAAGT AAGGAGCTCT CTTCAGCATC TGATGGTTAT ATTTTAAATC CAAAAGATAT 1080  
 CGTTGAAGAA ACGGCTACAG CTTATATTGT AAGACATGGT GATCATTTCC ATTACATTCC 1140  
 AAAATCAAAT CAAATTGGGC AACCGACTCT TCCAAACAAT AGTCTAGCAA CACCTTCTCC 1200  
 ATCTCTTCCA ATCAATCCAG GAACTTCACA TGAGAAACAT GAAGAAGATG GATACGGATT 1260  
 TGATGCTAAT CGTATTATCG CTGAAGATGA ATCAGGTTTT GTCATGAGTC ACGGAGACCA 1320  
 CAATCATTAT TTCTTCAAGA AG 1342

(2) INFORMATION FOR SEQ ID NO:182:


(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn Asn Arg Val Ser  
 1 5 10 15  
 Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu Asn Leu Thr Pro  
 20 25 30  
 Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu Gln Ile Val Ile  
 35 40 45  
 Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp His Tyr His  
 50 55 60  
 Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe Ser Glu Glu Leu  
 65 70 75 80  
 Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala Asp Ile Val Asn  
 85 90 95  
 Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly Lys Tyr Tyr Val  
 100 105 110  
 Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr Lys Asp Glu  
 115 120 125  
 Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn Glu Lys Val Asn  
 130 135 140



Ser	Asn	Val	Ala	Val	Ala	Arg	Ser	Gln	Gly	Arg	Tyr	Thr	Thr	Asn	Asp	145	150	155	160
Gly	Tyr	Val	Phe	Asn	Pro	Ala	Asp	Ile	Ile	Glu	Asp	Thr	Gly	Asn	Ala	165	170	175	
Tyr	Ile	Val	Pro	His	Gly	Gly	His	Tyr	His	Tyr	Ile	Pro	Lys	Ser	Asp	180	185	190	
Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala	Ala	Lys	Ala	His	Leu	Ala	Gly	Lys	195	200	205	
Asn	Met	Gln	Pro	Ser	Gln	Leu	Ser	Tyr	Ser	Ser	Thr	Ala	Ser	Asp	Asn	210	215	220	
Asn	Thr	Gln	Ser	Val	Ala	Lys	Gly	Ser	Thr	Ser	Lys	Pro	Ala	Asn	Lys	225	230	235	240
Ser	Glu	Asn	Leu	Gln	Ser	Leu	Leu	Lys	Glu	Leu	Tyr	Asp	Ser	Pro	Ser	245	250	255	
Ala	Gln	Arg	Tyr	Ser	Glu	Ser	Asp	Gly	Leu	Val	Phe	Asp	Pro	Ala	Lys	260	265	270	
Ile	Ile	Ser	Arg	Thr	Pro	Asn	Gly	Val	Ala	Ile	Pro	His	Gly	Asp	His	275	280	285	
Tyr	His	Phe	Ile	Pro	Tyr	Ser	Lys	Leu	Ser	Ala	Leu	Glu	Glu	Lys	Ile	290	295	300	
Ala	Arg	Met	Val	Pro	Ile	Ser	Gly	Thr	Gly	Ser	Thr	Val	Ser	Thr	Asn	305	310	315	320
Ala	Lys	Pro	Asn	Glu	Val	Val	Ser	Ser	Leu	Gly	Ser	Leu	Ser	Ser	Asn	325	330	335	
Pro	Ser	Ser	Leu	Thr	Thr	Ser	Lys	Glu	Leu	Ser	Ser	Ala	Ser	Asp	Gly	340	345	350	
Tyr	Ile	Phe	Asn	Pro	Lys	Asp	Ile	Val	Glu	Glu	Thr	Ala	Thr	Ala	Tyr	355	360	365	
Ile	Val	Arg	His	Gly	Asp	His	Phe	His	Tyr	Ile	Pro	Lys	Ser	Asn	Gln	370	375	380	
Ile	Gly	Gln	Pro	Thr	Leu	Pro	Asn	Asn	Ser	Leu	Ala	Thr	Pro	Ser	Pro	385	390	395	400
Ser	Leu	Pro	Ile	Asn	Pro	Gly	Thr	Ser	His	Glu	Lys	His	Glu	Glu	Asp	405	410	415	
Gly	Tyr	Gly	Phe	Asp	Ala	Asn	Arg	Ile	Ile	Ala	Glu	Asp	Glu	Ser	Gly	420	425	430	
Phe	Val	Met	Ser	His	Gly	Asp	His	Asn	His	Tyr	Phe	Phe	Lys	Lys		435	440	445	

## (2) INFORMATION FOR SEQ ID NO: 183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 934 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

TGACTACCTT GAAATCCAC TTTACAGCTA TCTTGGTGGA TTCAACACTA AAGTTCTTCC 60  
 AACTCCAATG ATGAACATCA TCAACGGTGG TTCTCACTCT GACGCTCCAA TCGCTTTCCA 120  
 AGAGTTCATG ATCTTGCCAG TTGGTGCGCC AACATTTAAA GAAGCCCTTC GTTACGGTGC 180  
 TGAAATCTTC CACGCTCTTA AGAAAATCCT TAAATCACGT GGT'TTGAAA CTGCCGTAGG 240  
 TGACGAAGGT GGATTCGCTC CTCGTTTCGA AGGAACTGAA GATGGTGTG AACTATCCT 300  
 TGCTGCGATT GAAGCTGCTG GATATGTACC AGGTAAAGAC GTATTTATCG GATTTGACTG 360  
 TGCTTCATCA GAATTCTACG ATAAAGAACG TAAAGTTTAC GACTACACTA AATTTGAAGG 420  
 TGAAGGTGCT GCTGTTTCGTA CATCTGCAGA ACAAATCGAC TACCTTGAAG AATTGGTTAA 480  
 CAAATACCCA ATCATCACTA TTGAAGATGG TATGGATGAA AACGACTGGG ATGGTTGGAA 540  
 AGCTCTTACT GAACGTCTTG GTAAGAAAGT ACAACTTGT'T GGTGACGACT TCTTCGTAAC 600  
 AAACACTGAC TACCTTGCAC GTGGTATCCA AGAAGGTGCT GCTAACTCAA TCCTTATCAA 660  
 AGTTAACCAA ATCGGTACTC TTACTGAAAC TTTTGAAGCT ATCGAAATGG CTAAAGAAGC 720  
 TGGTTACACT GCTGTTGTAT CACACCGTTC AGGTGAAACT GAAGATTCAA CAATCGCTGA 780  
 TATTGCAGTT GCAACTAACG CAGGACAAAT CAAGACTGGT TCACTTTCAC GTACAGACCG 840  
 CATCGCTAAA TACAACCAAT TGCTTCGTAT CGAAGACCAA CTTGGTGAAG TAGCTGAATA 900  
 TCGTGGATTG AAATCATTCT ACAACCTTAA AAAA 934

## (2) INFORMATION FOR SEQ ID NO:184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Asp Tyr Leu Glu Ile Pro Leu Tyr Ser Tyr Leu Gly Gly Phe Asn Thr  
 1 5 10 15  
 Lys Val Leu Pro Thr Pro Met Met Asn Ile Ile Asn Gly Gly Ser His  
 20 25 30  
 Ser Asp Ala Pro Ile Ala Phe Gln Glu Phe Met Ile Leu Pro Val Gly  
 35 40 45  
 Ala Pro Thr Phe Lys Glu Ala Leu Arg Tyr Gly Ala Glu Ile Phe His  
 50 55 60  
 Ala Leu Lys Lys Ile Leu Lys Ser Arg Gly Leu Glu Thr Ala Val Gly  
 65 70 75 80

Asp Glu Gly Gly Phe Ala Pro Arg Phe Glu Gly Thr Glu Asp Gly Val  
 85 90 95  
 Glu Thr Ile Leu Ala Ala Ile Glu Ala Ala Gly Tyr Val Pro Gly Lys  
 100 105 110  
 Asp Val Phe Ile Gly Phe Asp Cys Ala Ser Ser Glu Phe Tyr Asp Lys  
 115 120 125  
 Glu Arg Lys Val Tyr Asp Tyr Thr Lys Phe Glu Gly Glu Gly Ala Ala  
 130 135 140  
 Val Arg Thr Ser Ala Glu Gln Ile Asp Tyr Leu Glu Glu Leu Val Asn  
 145 150 155 160  
 Lys Tyr Pro Ile Ile Thr Ile Glu Asp Gly Met Asp Glu Asn Asp Trp  
 165 170 175  
 Asp Gly Trp Lys Ala Leu Thr Glu Arg Leu Gly Lys Lys Val Gln Leu  
 180 185 190  
 Val Gly Asp Asp Phe Phe Val Thr Asn Thr Asp Tyr Leu Ala Arg Gly  
 195 200 205  
 Ile Gln Glu Gly Ala Ala Asn Ser Ile Leu Ile Lys Val Asn Gln Ile  
 210 215 220  
 Gly Thr Leu Thr Glu Thr Phe Glu Ala Ile Glu Met Ala Lys Glu Ala  
 225 230 235 240  
 Gly Tyr Thr Ala Val Val Ser His Arg Ser Gly Glu Thr Glu Asp Ser  
 245 250 255  
 Thr Ile Ala Asp Ile Ala Val Ala Thr Asn Ala Gly Gln Ile Lys Thr  
 260 265 270  
 Gly Ser Leu Ser Arg Thr Asp Arg Ile Ala Lys Tyr Asn Gln Leu Leu  
 275 280 285  
 Arg Ile Glu Asp Gln Leu Gly Glu Val Ala Glu Tyr Arg Gly Leu Lys  
 290 295 300  
 Ser Phe Tyr Asn Leu Lys Lys  
 305 310

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

TCGTATCTTT TTTTGGAGCA ATGTTGCGGT AGAAGGACAT TCCATGGATC CGACCCTAGC	60
GGATGGCGAA ATTCTCTTCG TTGTAAAACA CCTTCCTATT GACCGTTTGT ATATCGTGGT	120
GGCCCATGAG GAAGATGGCA ATAAGGACAT CGTCAAGCGC GTGATTGGAA TGCCTGGCGA	180

CACCATTCGT TACGAAAATG ATAAACTCTA CATCAATGAC AAAGAAACGG ACGAGCCTTA 240  
 TCTAGCAGAC TATATCAAAC GCTTCAAGGA TGACAAACTC CAAAGCACTT ACTCAGGCAA 300  
 GGGCTTTTGA GAAATAAAG GAACTTTCTT TAGAAGTATC GCTCAAAAAG CTCAAGCCTT 360  
 CACAGTTGAT GTCAACTACA ACACCAACTT TAGCTTTACT GTTCCAGAAG GAGAATACCT 420  
 TCTCCTCGGA GATGACCGCT TGGTTTCGAG CGACAGCCGC CACGTAGGTA CCTTCAAAGC 480  
 AAAAGATATC ACAGGGGAAG CTAAATTCCG CTTATGGCCA ATCACCCGTA TCGGAACATT 540  
 T 541

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg Ile Phe Phe Trp Ser Asn Val Arg Val Glu Gly His Ser Met Asp  
 1 5 10 15  
 Pro Thr Leu Ala Asp Gly Glu Ile Leu Phe Val Val Lys His Leu Pro  
 20 25 30  
 Ile Asp Arg Phe Asp Ile Val Val Ala His Glu Glu Asp Gly Asn Lys  
 35 40 45  
 Asp Ile Val Lys Arg Val Ile Gly Met Pro Gly Asp Thr Ile Arg Tyr  
 50 55 60  
 Glu Asn Asp Lys Leu Tyr Ile Asn Asp Lys Glu Thr Asp Glu Pro Tyr  
 65 70 75 80  
 Leu Ala Asp Tyr Ile Lys Arg Phe Lys Asp Asp Lys Leu Gln Ser Thr  
 85 90 95  
 Tyr Ser Gly Lys Gly Phe Glu Gly Asn Lys Gly Thr Phe Phe Arg Ser  
 100 105 110  
 Ile Ala Gln Lys Ala Gln Ala Phe Thr Val Asp Val Asn Tyr Asn Thr  
 115 120 125  
 Asn Phe Ser Phe Thr Val Pro Glu Gly Glu Tyr Leu Leu Leu Gly Asp  
 130 135 140  
 Asp Arg Leu Val Ser Ser Asp Ser Arg His Val Gly Thr Phe Lys Ala  
 145 150 155 160  
 Lys Asp Ile Thr Gly Glu Ala Lys Phe Arg Leu Trp Pro Ile Thr Arg  
 165 170 175  
 Ile Gly Thr Phe  
 180

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```


GGACTCTCTC AAAGATGTGA AAGCAAATGC TAGCGACAGC AAGCCTGCAC AGGACAAGAA      60
GGATGCAAAA CAAGGAACGG AAGATAGTAA GGATTCAGAT AAGATGACTG AAACAAACTC      120
AGTTCCGGCA GGAGTGATTG TGGTCAGTCT ACTTGCCCTC CTAGGCGTGA TTGCCTTCTG      180
GCTGATTTCG CGTAAGAAAG AGTCAGAAAT CCAGCAATTA AGCACGGAAT TGATCAAGGT      240
TCTAGGACAG CTAGATGCAG AAAAAGCGGA TAAAAAGTC CTTGCCAAAG CCCAAAACCT      300
TCTCCAAGAA ACCCTTGATT TCGTGAAAGA AGAAAATGGC TCAGCAGAGA CAGAAACTAA      360
ACTAGTAGAG GAGCTTAAAG CAATCCTTGA CAAACTCAAG      400
  
```

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 133 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:



```

Asp Ser Leu Lys Asp Val Lys Ala Asn Ala Ser Asp Ser Lys Pro Ala
1      5      10      15
Gln Asp Lys Lys Asp Ala Lys Gln Gly Thr Glu Asp Ser Lys Asp Ser
20     25     30
Asp Lys Met Thr Glu Thr Asn Ser Val Pro Ala Gly Val Ile Val Val
35     40     45
Ser Leu Leu Ala Leu Leu Gly Val Ile Ala Phe Trp Leu Ile Arg Arg
50     55     60
Lys Lys Glu Ser Glu Ile Gln Gln Leu Ser Thr Glu Leu Ile Lys Val
65     70     75     80
Leu Gly Gln Leu Asp Ala Glu Lys Ala Asp Lys Lys Val Leu Ala Lys
85     90     95
Ala Gln Asn Leu Leu Gln Glu Thr Leu Asp Phe Val Lys Glu Glu Asn
100    105    110
Gly Ser Ala Glu Thr Glu Thr Lys Leu Val Glu Glu Leu Lys Ala Ile
115    120    125
Leu Asp Lys Leu Lys
130
  
```

## (2) INFORMATION FOR SEQ ID NO: 189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

CAAGAAATCC TATCATCTCT TCCAGAAGCA AACAGAGACG AGGGGAATTC AGACTCAGTT 60  
 GATTGAAGAA TCGCTTAGTC AGCAGACTAT AATCCAGTCC TTCAATGCTC AAACAGAATT 120  
 TATCCAAAGA TTGCGTGAGG CTCATGACAA CTACTCAGGC TATTCTCAGT CAGCCATCTT 180  
 TTATTCTTCA ACGGTCAATC CTTGACTCG CTTTGTAAT GCACTCATTT ATGCCCTTTT 240  
 AGCTGGAGTA GGAGCTTATC GTATCATGAT GGGTTCAGCC TTGACCGTCG GTCGTTTAGT 300  
 GACTTTTTTG AACTATGTTC AGCAATACAC CAAGCCCTTT AACGATATTT CTTCAGTGCT 360  
 AGCTGAGTTG CAAAGTGCTC TGGCTTGCGT AGAGCGTATC TATGGAGTCT TAGATAGCCC 420  
 TGAAGTGGCT GAAACAGGTA AGGAAGTCTT GACGACCAGT GACCAAGTTA AGGGAGCTAT 480  
 TTCCTTTAAA CATGTCTCTT TTGGCTACCA TCCTGAAAAA ATTTTGATTA AGGACTTGTC 540  
 TATCGATATT CCAGCTGGTA GTAAGGTAGC CATCGTTGGT CCGACAGGTG CTGGAAAATC 600  
 AACTCTTATC AATCTCCTTA TGCCTTTTTA TCCCATTAGC TCGGGAGATA TCTTGCTGGA 660  
 TGGGCAATCC ATTTATGATT ATACACGAGT ATCATTGAGA CAGCAGTTTG GTATGGTGCT 720  
 TCAAGAAACC TGGCTCACAC AAGGGACCAT TCATGATAAT ATTGCCCTTTG GCAATCCTGA 780  
 AGCCAGTCGA GAGCAAGTAA TTGCTGCTGC CAAAGCAGCT AATGCAGACT TTTTCATCCA 840  
 ACAGTTGCCA CAGGGATACG ATACCAAGTT GGAAAATGCT GGAGAATCTC TCTCTGTCGG 900  
 CCAAGCTCAG CTCTTGACCA TAGCCCGAGT CTTTCTGGCT ATTCCAAAGA TTCTTATCTT 960  
 AGACGAGGCA ACTTCTTCCA TTGATACACG GACAGAAGTG CTGGTACAGG ATGCCCTTTGC 1020  
 AAAACTCATG AAGGGCCGCA CAAGTTTCAT CATTGCTCAC CGTTTGTCAG CCATTCAGGA 1080  
 TGCGGATTTA ATTCTTGTCT TAGTAGATGG TGATATTGTT GAATATGGTA ACCATCAAGA 1140  
 ACTCATGGAT AGAAAGGGTA AGTATTACCA AATGCAAAAA GCTGCGGCTT TTAGTTCTGA 1200  
 A 1201

## (2) INFORMATION FOR SEQ ID NO:190:


## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:



Lys	Lys	Ser	Tyr	His	Leu	Phe	Gln	Lys	Gln	Thr	Glu	Thr	Arg	Gly	Ile
1				5					10					15	
Gln	Thr	Gln	Leu	Ile	Glu	Glu	Ser	Leu	Ser	Gln	Gln	Thr	Ile	Ile	Gln
			20					25					30		
Ser	Phe	Asn	Ala	Gln	Thr	Glu	Phe	Ile	Gln	Arg	Leu	Arg	Glu	Ala	His
		35					40					45			
Asp	Asn	Tyr	Ser	Gly	Tyr	Ser	Gln	Ser	Ala	Ile	Phe	Tyr	Ser	Ser	Thr
	50					55					60				
Val	Asn	Pro	Ser	Thr	Arg	Phe	Val	Asn	Ala	Leu	Ile	Tyr	Ala	Leu	Leu
65					70					75					80
Ala	Gly	Val	Gly	Ala	Tyr	Arg	Ile	Met	Met	Gly	Ser	Ala	Leu	Thr	Val
				85					90					95	
Gly	Arg	Leu	Val	Thr	Phe	Leu	Asn	Tyr	Val	Gln	Gln	Tyr	Thr	Lys	Pro
			100					105					110		
Phe	Asn	Asp	Ile	Ser	Ser	Val	Leu	Ala	Glu	Leu	Gln	Ser	Ala	Leu	Ala
		115					120					125			
Cys	Val	Glu	Arg	Ile	Tyr	Gly	Val	Leu	Asp	Ser	Pro	Glu	Val	Ala	Glu
	130					135					140				
Thr	Gly	Lys	Glu	Val	Leu	Thr	Thr	Ser	Asp	Gln	Val	Lys	Gly	Ala	Ile
145					150					155					160
Ser	Phe	Lys	His	Val	Ser	Phe	Gly	Tyr	His	Pro	Glu	Lys	Ile	Leu	Ile
				165					170					175	
Lys	Asp	Leu	Ser	Ile	Asp	Ile	Pro	Ala	Gly	Ser	Lys	Val	Ala	Ile	Val
			180					185					190		
Gly	Pro	Thr	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Ile	Asn	Leu	Leu	Met	Arg
		195					200					205			
Phe	Tyr	Pro	Ile	Ser	Ser	Gly	Asp	Ile	Leu	Leu	Asp	Gly	Gln	Ser	Ile
	210					215					220				
Tyr	Asp	Tyr	Thr	Arg	Val	Ser	Leu	Arg	Gln	Gln	Phe	Gly	Met	Val	Leu
225					230					235					240
Gln	Glu	Thr	Trp	Leu	Thr	Gln	Gly	Thr	Ile	His	Asp	Asn	Ile	Ala	Phe
				245					250					255	
Gly	Asn	Pro	Glu	Ala	Ser	Arg	Glu	Gln	Val	Ile	Ala	Ala	Ala	Lys	Ala
			260					265					270		
Ala	Asn	Ala	Asp	Phe	Phe	Ile	Gln	Gln	Leu	Pro	Gln	Gly	Tyr	Asp	Thr
		275					280					285			
Lys	Leu	Glu	Asn	Ala	Gly	Glu	Ser	Leu	Ser	Val	Gly	Gln	Ala	Gln	Leu
	290					295					300				
Leu	Thr	Ile	Ala	Arg	Val	Phe	Leu	Ala	Ile	Pro	Lys	Ile	Leu	Ile	Leu
305					310					315					320

Asp Glu Ala Thr Ser Ser Ile Asp Thr Arg Thr Glu Val Leu Val Gln  
 325 330 335

Asp Ala Phe Ala Lys Leu Met Lys Gly Arg Thr Ser Phe Ile Ile Ala  
 340 345 350

His Arg Leu Ser Thr Ile Gln Asp Ala Asp Leu Ile Leu Val Leu Val  
 355 360 365

Asp Gly Asp Ile Val Glu Tyr Gly Asn His Gln Glu Leu Met Asp Arg  
 370 375 380

Lys Gly Lys Tyr Tyr Gln Met Gln Lys Ala Ala Ala Phe Ser Ser Glu  
 385 390 395 400

## (2) INFORMATION FOR SEQ ID NO: 191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ACGAAATGCA GGGCAGACAG ATGCCCTCGCA AATTGAAAAG GCGGCAGTTA GCCAAGGAGG 60

AAAAGCAGTG AAAAAACAG AAATTAGTAA AGACGCAGAC TTGCACGAAA TTTATCTAGC 120

TGGAGGTTGT TTCTGGGGAG TGGAGGAATA TTTCTCACGT GTTCCCGGGG TGACGGATGC 180

CGTTTCAGGC TATGCAAATG GTAGAGGAGA AACAACCAAG TACGAATTGA TTAACCAAAC 240

AGGTCATGCA GAAACCGTCC ATGTCACCTA TGATGCCAAG CAAATTTCTC TCAAGGAAAT 300

CCTGCTTCAC TATTTCCGCA TTATCAATCC AACCAGCAAA AATAACAAG GAAATGATGT 360

GGGGACCCAG TACCGTACTG GTGTTTATTA CACAGATGAC AAGGATTGG AAGTGATTAA 420

CCAAGTCTTT GATGAGGTGG CTAAGAAATA CGATCAACCT CTAGCAGTTG AAAAGGAAAA 480

CTTGAAGAAT TTTGTGGTGG CTGAGGATTA CCATCAAGAC TATCTCAAGA AAAATCCAAA 540

TGGCTACTGC CATATCAATG TTAATCAGGC GGCCTATCCT GTCATTGATG CCAGCAAATA 600

TCCAAAACCA AGTGATGAGG AATTGAAAAA GACCCTGTCA CCTGAGGAGT ATGCAGTTAC 660

CCAGGAAAAT CAAACAGAAC GAGCTTTCTC AAACCGTTAC TGGGATAAAT TTGAATCCGG 720

TATCTATGTG GATATAGCAA CTGGGGAACC TCTCTTTTCA TCAAAAGACA AATTTGAGTC 780

TGGTTGTGGC TGGCCTAGTT TTACCCAACC CATCAGTCCA GATGTTGTCA CCTACAAGGA 840

AGATAAGTCC TACAATATGA CGCGTATGGA AGTGCGGAGC CGAGTAGGAG ATTCTCACCT 900

TGGGCATGTC TTTACGGATG GTCCACAGGA CAAGGGCGGC TTACGTTACT GTATCAATAG 960

CCTCTCTATC CGCTTTATTC CCAAAGACCA AATGGAAGAA AAAGGCTACG CTTATTTACT 1020

AGATTATGTT GAT 1033

## (2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 344 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Arg Asn Ala Gly Gln Thr Asp Ala Ser Gln Ile Glu Lys Ala Ala Val  
 1 5 10 15  
 Ser Gln Gly Gly Lys Ala Val Lys Lys Thr Glu Ile Ser Lys Asp Ala  
 20 25 30  
 Asp Leu His Glu Ile Tyr Leu Ala Gly Gly Cys Phe Trp Gly Val Glu  
 35 40 45  
 Glu Tyr Phe Ser Arg Val Pro Gly Val Thr Asp Ala Val Ser Gly Tyr  
 50 55 60  
 Ala Asn Gly Arg Gly Glu Thr Thr Lys Tyr Glu Leu Ile Asn Gln Thr  
 65 70 75 80  
 Gly His Ala Glu Thr Val His Val Thr Tyr Asp Ala Lys Gln Ile Ser  
 85 90 95  
 Leu Lys Glu Ile Leu Leu His Tyr Phe Arg Ile Ile Asn Pro Thr Ser  
 100 105 110  
 Lys Asn Lys Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg Thr Gly Val  
 115 120 125  
 Tyr Tyr Thr Asp Asp Lys Asp Leu Glu Val Ile Asn Gln Val Phe Asp  
 130 135 140  
 Glu Val Ala Lys Lys Tyr Asp Gln Pro Leu Ala Val Glu Lys Glu Asn  
 145 150 155 160  
 Leu Lys Asn Phe Val Val Ala Glu Asp Tyr His Gln Asp Tyr Leu Lys  
 165 170 175  
 Lys Asn Pro Asn Gly Tyr Cys His Ile Asn Val Asn Gln Ala Ala Tyr  
 180 185 190  
 Pro Val Ile Asp Ala Ser Lys Tyr Pro Lys Pro Ser Asp Glu Glu Leu  
 195 200 205  
 Lys Lys Thr Leu Ser Pro Glu Glu Tyr Ala Val Thr Gln Glu Asn Gln  
 210 215 220  
 Thr Glu Arg Ala Phe Ser Asn Arg Tyr Trp Asp Lys Phe Glu Ser Gly  
 225 230 235 240  
 Ile Tyr Val Asp Ile Ala Thr Gly Glu Pro Leu Phe Ser Ser Lys Asp  
 245 250 255  
 Lys Phe Glu Ser Gly Cys Gly Trp Pro Ser Phe Thr Gln Pro Ile Ser  
 260 265 270  
 Pro Asp Val Val Thr Tyr Lys Glu Asp Lys Ser Tyr Asn Met Thr Arg

275	280	285
Met Glu Val Arg Ser Arg Val Gly Asp Ser His Leu Gly His Val Phe		
290	295	300
Thr Asp Gly Pro Gln Asp Lys Gly Gly Leu Arg Tyr Cys Ile Asn Ser		
305	310	315
Leu Ser Ile Arg Phe Ile Pro Lys Asp Gln Met Glu Glu Lys Gly Tyr		
	325	330
Ala Tyr Leu Leu Asp Tyr Val Asp		
340		

## (2) INFORMATION FOR SEQ ID NO: 193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:



TGTATAGTTT TTAGCGCTTG TTCTTCTAAT TCTGNTAAAA ATGAAGAAAA TACTTCTAAA	60
GAGCATGCGC CTGATAAAAT AGTTTGTAGAT CATGCTTTTCG GTCAAACCTAT ATTAGATAAA	120
AAACCTGAAA GAGTTGCAAC TATTGCTTGG GGAAATCATG ATGTAGCATT AGCTTTAGGA	180
ATAGTTCCTG TTGGATTTTC AAAAGCAAAT TACGGTGTAAG GTGCTGATAA AGGAGTTTGA	240
CCATGGACAG AAGAAAAAAT CAAAGAACTA AATGGTAAAG CTAACCTATT TGACGATTTG	300
GATGGACTTA ACTTTGAAGC AATATCAAAT TCTAAACCAG ATGTTATCTT AGCAGGTTAT	360
TCTGGTATAA CTAAAGAAGA TTATGACACT CTATCA	396

## (2) INFORMATION FOR SEQ ID NO:194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Cys Ile Val Phe Ser Ala Cys Ser Ser Asn Ser Xaa Lys Asn Glu Glu	
1	5 10 15
Asn Thr Ser Lys Glu His Ala Pro Asp Lys Ile Val Leu Asp His Ala	
	20 25 30
Phe Gly Gln Thr Ile Leu Asp Lys Lys Pro Glu Arg Val Ala Thr Ile	
	35 40 45
Ala Trp Gly Asn His Asp Val Ala Leu Ala Leu Gly Ile Val Pro Val	
50	55 60

Gly Phe Ser Lys Ala Asn Tyr Gly Val Ser Ala Asp Lys Gly Val Leu  
 65 70 75 80  
 Pro Trp Thr Glu Glu Lys Ile Lys Glu Leu Asn Gly Lys Ala Asn Leu  
 85 90 95  
 Phe Asp Asp Leu Asp Gly Leu Asn Phe Glu Ala Ile Ser Asn Ser Lys  
 100 105 110  
 Pro Asp Val Ile Leu Ala Gly Tyr Ser Gly Ile Thr Lys Glu Asp Tyr  
 115 120 125  
 Asp Thr Leu Ser  
 130

## (2) INFORMATION FOR SEQ ID NO: 195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

GTGTGTCGAG CATATTCTGA AGCAAACCTA TCAAAATATA GAAATTATTT TAGTTGATGA 60  
 CGGTTCTACG GATAATTCTG GGGAAATTTG TGATGCTTTT ATGATGCAAG ATAATCGTGT 120  
 GCGAGTATTG CATCAAGAAA ATAAGGGGGG GGCAGCACAA GCTAAAAATA TGGGGATTAG 180  
 TGTAGCTAAG GGAGAGTACA TCACGATTGT TGATTGAGAT GATATCGTAA AAGAAAATAT 240  
 GATTGAAACT CTTTATCAGC AAGTCCAAGA AAAGGATGCA GATGTTGTTA TAGGGAATTA 300  
 CTATAATTAT GACGAAAGTG ACGGGAATTT TTATTTTTTAT GTAACAGGGC AAGATTTTTG 360  
 CGTCGAAGAA TTAGCTATAC AAGAAATTAT GAACCGTCAA GCAGGAGATT GGAAATTCAA 420  
 TAGCTCGGCC TTTATATTGC CGACATTTAA GTTGATTAAA AAAGAATTAT TCAATGAAGT 480  
 TCACTTTTCA AATGGTCGCC GCTTTGATGA TGAAGCAACT ATGCATCGCT TTTATCTTTT 540  
 AGCCTCTAAA ATCGTCTTTA TAAACGATAA TCTCTATCTG TATAGAAGAC GTTCAGGAAG 600  
 CATCATGAGA ACGGAATTTG ATCTTTCCCTG GGCAAGAGAT ATTGTTGAAG TGTTTTCTAA 660  
 GAAAATATCG GATTGTGTCT TGGCTGGTTT GGATGTCTCC GTTCTGCGTA TTCGATTTGT 720  
 CAATCTTTTA AAAGATTATA AGCAAAC'TTT AGAATACCAT CAATTAACAG ATACTGAGGA 780  
 ATATAAAGAT ATTTGTTTCA GATTAAAGTT GTTTTTTGAT GCAGAACAAA GAAATGGTAA 840  
 AAGT 844

## (2) INFORMATION FOR SEQ ID NO:196:


## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:



Cys	Val	Glu	His	Ile	Leu	Lys	Gln	Thr	Tyr	Gln	Asn	Ile	Glu	Ile	Ile	1	5	10	15
Leu	Val	Asp	Asp	Gly	Ser	Thr	Asp	Asn	Ser	Gly	Glu	Ile	Cys	Asp	Ala	20	25	30	
Phe	Met	Met	Gln	Asp	Asn	Arg	Val	Arg	Val	Leu	His	Gln	Glu	Asn	Lys	35	40	45	
Gly	Gly	Ala	Ala	Gln	Ala	Lys	Asn	Met	Gly	Ile	Ser	Val	Ala	Lys	Gly	50	55	60	
Glu	Tyr	Ile	Thr	Ile	Val	Asp	Ser	Asp	Asp	Ile	Val	Lys	Glu	Asn	Met	65	70	75	80
Ile	Glu	Thr	Leu	Tyr	Gln	Gln	Val	Gln	Glu	Lys	Asp	Ala	Asp	Val	Val	85	90	95	
Ile	Gly	Asn	Tyr	Tyr	Asn	Tyr	Asp	Glu	Ser	Asp	Gly	Asn	Phe	Tyr	Phe	100	105	110	
Tyr	Val	Thr	Gly	Gln	Asp	Phe	Cys	Val	Glu	Glu	Leu	Ala	Ile	Gln	Glu	115	120	125	
Ile	Met	Asn	Arg	Gln	Ala	Gly	Asp	Trp	Lys	Phe	Asn	Ser	Ser	Ala	Phe	130	135	140	
Ile	Leu	Pro	Thr	Phe	Lys	Leu	Ile	Lys	Lys	Glu	Leu	Phe	Asn	Glu	Val	145	150	155	160
His	Phe	Ser	Asn	Gly	Arg	Arg	Phe	Asp	Asp	Glu	Ala	Thr	Met	His	Arg	165	170	175	
Phe	Tyr	Leu	Leu	Ala	Ser	Lys	Ile	Val	Phe	Ile	Asn	Asp	Asn	Leu	Tyr	180	185	190	
Leu	Tyr	Arg	Arg	Arg	Ser	Gly	Ser	Ile	Met	Arg	Thr	Glu	Phe	Asp	Leu	195	200	205	
Ser	Trp	Ala	Arg	Asp	Ile	Val	Glu	Val	Phe	Ser	Lys	Lys	Ile	Ser	Asp	210	215	220	
Cys	Val	Leu	Ala	Gly	Leu	Asp	Val	Ser	Val	Leu	Arg	Ile	Arg	Phe	Val	225	230	235	240
Asn	Leu	Leu	Lys	Asp	Tyr	Lys	Gln	Thr	Leu	Glu	Tyr	His	Gln	Leu	Thr	245	250	255	
Asp	Thr	Glu	Glu	Tyr	Lys	Asp	Ile	Cys	Phe	Arg	Leu	Lys	Leu	Phe	Phe	260	265	270	
Asp	Ala	Glu	Gln	Arg	Asn	Gly	Lys	Ser								275	280		

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GTGTTTGGAT AGCATTTCAGA ATCAGACGTA TCAAAATTTT GAGTGTTTAT TAATCAATGA 60  
 TGGCTCTCCA GATCATTCAT CCAAAATATG TGAAGAATTT GTAGAGAAAG ATTCTCGTTT 120  
 CAAATATTTT GAGAAAGCAA ACGGCGGTCT TTCATCAGCT CGTAACCTAG GTATTGAATG 180  
 TTCGGGGGGG GCGTACATTA CTTTTGTAGA CTCTGATGAT TGGTTGGAAC ATGATGCTTT 240  
 AGACCGATTA TATGGTGCCTT TGAAAAAGGA AAACGCAGAT ATTAGTATCG GGC GTTATAA 300  
 TTCTTATGAT GAAACACGCT ATGTGTATAT GACTTATGTT ACGGATCCAG ATGATTCTCT 360  
 AGAAGTGATA GAAGGTAAAG CAATTATGGA TAGGGAAGGT GTCGAAGAAG TCAGAAATGG 420  
 GAACTGGACT GTAGCTGTCT TGAAGTTATT CAAGAGAGAG TTA CTACAAG ATTTACCATT 480  
 TCCTATAGGA AAAATTGCAG AGGATACTTA CTGGACATGG AAGGTACTTC TAAGAGCTTC 540  
 GAGGATAGTC TATTTGAATC GTTGTGTTTA CTGGTACCGT GTTGGTTTAT CTGATACTTT 600  
 ATCGAATACA TGGAGTGAAA AGCGTATGTA TGATGAAATT GGGGCTAGGG AAGAAAAGAT 660  
 AGCTATTTTA GCAAGTTCAG ACTATGACTT GACCAATCAT ATTTTGATTT ATAAAAATAG 720  
 ATTACAAAGA GTGATAGCAA AATTAGAAGA ACAAATATG CAGTTCACAG AGATTTACAG 780  
 AAGAATGATG GAAAAATTGT CTTTACTTCC G 811

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 270 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Cys Leu Asp Ser Ile Gln Asn Gln Thr Tyr Gln Asn Phe Glu Cys Leu  
 1 5 10 15  
 Leu Ile Asn Asp Gly Ser Pro Asp His Ser Ser Lys Ile Cys Glu Glu  
 20 25 30  
 Phe Val Glu Lys Asp Ser Arg Phe Lys Tyr Phe Glu Lys Ala Asn Gly  
 35 40 45  
 Gly Leu Ser Ser Ala Arg Asn Leu Gly Ile Glu Cys Ser Gly Gly Ala  
 50 55 60  
 Tyr Ile Thr Phe Val Asp Ser Asp Asp Trp Leu Glu His Asp Ala Leu  
 65 70 75 80

Asp Arg Leu Tyr Gly Ala Leu Lys Lys Glu Asn Ala Asp Ile Ser Ile  
 85 90 95  
 Gly Arg Tyr Asn Ser Tyr Asp Glu Thr Arg Tyr Val Tyr Met Thr Tyr  
 100 105 110  
 Val Thr Asp Pro Asp Asp Ser Leu Glu Val Ile Glu Gly Lys Ala Ile  
 115 120 125  
 Met Asp Arg Glu Gly Val Glu Glu Val Arg Asn Gly Asn Trp Thr Val  
 130 135 140  
 Ala Val Leu Lys Leu Phe Lys Arg Glu Leu Leu Gln Asp Leu Pro Phe  
 145 150 155 160  
 Pro Ile Gly Lys Ile Ala Glu Asp Thr Tyr Trp Thr Trp Lys Val Leu  
 165 170 175  
 Leu Arg Ala Ser Arg Ile Val Tyr Leu Asn Arg Cys Val Tyr Trp Tyr  
 180 185 190  
 Arg Val Gly Leu Ser Asp Thr Leu Ser Asn Thr Trp Ser Glu Lys Arg  
 195 200 205  
 Met Tyr Asp Glu Ile Gly Ala Arg Glu Glu Lys Ile Ala Ile Leu Ala  
 210 215 220  
 Ser Ser Asp Tyr Asp Leu Thr Asn His Ile Leu Ile Tyr Lys Asn Arg  
 225 230 235 240  
 Leu Gln Arg Val Ile Ala Lys Leu Glu Glu Gln Asn Met Gln Phe Thr  
 245 250 255  
 Glu Ile Tyr Arg Arg Met Met Glu Lys Leu Ser Leu Leu Pro  
 260 265 270

## (2) INFORMATION FOR SEQ ID NO: 199:


## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GTGCCTAGAT AGTATTATTA CTCAAACATA TAAAAATATT GAGATTGTTG TCGTTAATGA	60
TGGTTCTACG GATGCTTCAG GTGAAATTTG TAAAGAATTT TCAGAAATGG ATCACCGAAT	120
TCTCTATATA GAACAAGAAA ATGCTGGTCT TTCTGCCGCA CGAAACACCG GTCTGAATAA	180
TATGTCCGGA AATTATGTGA CCTTTGTGGA CTCGGATGAT TGGATTGAGC AAGATTATGT	240
AGAAACTCTA TATAAAAAAA TAGTAGAGTA TCAGGCTGAT ATTGCAGTTG GTAATTATTA	300
TTCTTTCAAC GAAAGTGAAG GAATGTTCTA CTTTCATATA TTGGGAGACT CCTATTATGA	360
GAAAGTATAT GATAATGTTT CTATCTTTGA GAAC TTGTAT GAAACTCAAG AAATGAAGAG	420
TTTTGCTTTG ATATCTGCTT GGGGTAAACT CTATAAGGCA AGATTGTTTG AGCAGTTGCC	480





CTTTGACATA	GGTAAATTAG	GAGAAGATGG	TTACCTCAAT	CAAAAGGTAT	ATTTATTATC	540
AGAAAAGGTA	ATTTATTTAA	ATAAAAGTCT	TTATGCTTAT	CGGATTAGAA	AAGGTAGTTT	600
ATCAAGAGTT	TGGACAGAAA	AGTGGATGCA	CGCTTTAGTT	GATGCTATGT	CTGAACGTAT	660
TACGCTACTA	GCTAATATGG	GTTATCCTCT	AGAGAAACAC	TTGGCAGTTT	ATCGTCAGAT	720
GTTGGAAGTC	AGTCTCGCCA	ACGGTCAAGC	TAGTGGTTTA	TCTGACACAG	CAACGTATAA	780
AGAGTTTGAA	ATGAAACAAA	GGCTTTTAAA	TCAGCTATCG	AGACAAGAGG	AAAGTGAAAA	840
GAAAGCCATT	GTCCTCGCAG	CAAACATATG	CTATGTAGAC	CAAGTTTTAA	CGACAATCAA	900
GTCTATTTGT	TATCATAATC	GTTTCGATTC	TTTTTATCTG	ATTCATAGCG	ATTTTCCAAA	960
TGAATGGATT	AAGCAATTAA	ATAAGCGCTT	AGAGAAGTTT	GACTCAGAAA	TTATTAATTG	1020
TCGGGTAACT	TCTGAGCAAA	TTTCATGTTA	TAAATCGGAT	ATTAGTTACA	CAGTCTTTTTT	1080
ACGCTATTTT	ATAGCTGATT	TCGTGCAAGA	AGACAAGGCC	CTCTACTTGG	ACTGTGATCT	1140
AGTTGTAACG	AAAAATCTGG	ATGACTTGTT	TGCTACAGAC	TTACAAGATT	ATCCTTTGGC	1200
TGCTGTTAGA	GATTTTGGGG	GCAGAGCTTA	TTTTGGTCAA	GAAATCTTTA	ATGCCGGTGT	1260
TCTCTTGGTA	AACAATGCTT	TTTGAAAAAA	AGAGAATATG	ACCCAAAAAT	TAATTGATGT	1320
AACCAATGAA	TGGCATGATA	AGGTGGATCA	GGCAGATCAG	AGCATCTTGA	ATATGCTTTT	1380
TGAACATAAA	TGGTTGGAAT	TGGACTTTGA	TTATAATCAT	ATTGTCATTC	ATAAACAGTT	1440
TGCTGATTAT	CAATTGCCTG	AGGGTCAGGA	TTATCCTGCT	ATTATTCACT	ATCTTTCTCA	1500
TCGGAAACCG	TGGAAAGATT	TGGCGGCCCA	AACCTATCGT	GAAGTTTGGT	GGTACTATCA	1560
TGGGCTTGAA	TGGACAGAAT	TGGGACAAAA	CCATCATTTA	CATCCATTAC	AAAGATCTCA	1620
CATCTATCCA	ATAAAGGAAC	CTTTCACCTG	TCTAATCTAT	ACTGCCTCAG	ACCATATTGA	1680
ACAAATTGAG	ACATTGGTTC	AATCCTTGCC	TGATATTGAG	TTTAAGATAG	CAGCTAGAGT	1740
AATAGTTAGT	GATCGATTGG	CTCAGATGAC	AATTTATCCA	AACGTGACTA	TATTTAACGG	1800
AATTCATAT	TTGGTAGATG	TCGATAATGA	ATTGGTAGAA	ACCAGTCAAG	TACTTTTAGA	1860
TATTAATCAT	GGCGAAAAGA	CAGAAGAAAT	TCTCGATCAA	TTTGCTAATC	TTGGCAAGCC	1920
TATCTTATCC	TTTGAAAATA	CTAAAACCTA	TGAAGTAGGT	CAGGAGGCAT	ATGCTGTTGA	1980
CCAAGTTCAA	GCAATGATTG	AAAAATTGAG	AGAAATAAGC	AAA		2023


## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:



Cys	Leu	Asp	Ser	Ile	Ile	Thr	Gln	Thr	Tyr	Lys	Asn	Ile	Glu	Ile	Val
1				5					10					15	
Val	Val	Asn	Asp	Gly	Ser	Thr	Asp	Ala	Ser	Gly	Glu	Ile	Cys	Lys	Glu
			20					25					30		
Phe	Ser	Glu	Met	Asp	His	Arg	Ile	Leu	Tyr	Ile	Glu	Gln	Glu	Asn	Ala
		35					40					45			
Gly	Leu	Ser	Ala	Ala	Arg	Asn	Thr	Gly	Leu	Asn	Asn	Met	Ser	Gly	Asn
	50					55					60				
Tyr	Val	Thr	Phe	Val	Asp	Ser	Asp	Asp	Trp	Ile	Glu	Gln	Asp	Tyr	Val
65					70					75					80
Glu	Thr	Leu	Tyr	Lys	Lys	Ile	Val	Glu	Tyr	Gln	Ala	Asp	Ile	Ala	Val
				85					90					95	
Gly	Asn	Tyr	Tyr	Ser	Phe	Asn	Glu	Ser	Glu	Gly	Met	Phe	Tyr	Phe	His
			100					105					110		
Ile	Leu	Gly	Asp	Ser	Tyr	Tyr	Glu	Lys	Val	Tyr	Asp	Asn	Val	Ser	Ile
		115					120					125			
Phe	Glu	Asn	Leu	Tyr	Glu	Thr	Gln	Glu	Met	Lys	Ser	Phe	Ala	Leu	Ile
	130					135					140				
Ser	Ala	Trp	Gly	Lys	Leu	Tyr	Lys	Ala	Arg	Leu	Phe	Glu	Gln	Leu	Arg
145					150					155					160
Phe	Asp	Ile	Gly	Lys	Leu	Gly	Glu	Asp	Gly	Tyr	Leu	Asn	Gln	Lys	Val
				165					170					175	
Tyr	Leu	Leu	Ser	Glu	Lys	Val	Ile	Tyr	Leu	Asn	Lys	Ser	Leu	Tyr	Ala
			180					185					190		
Tyr	Arg	Ile	Arg	Lys	Gly	Ser	Leu	Ser	Arg	Val	Trp	Thr	Glu	Lys	Trp
		195					200					205			
Met	His	Ala	Leu	Val	Asp	Ala	Met	Ser	Glu	Arg	Ile	Thr	Leu	Leu	Ala
	210					215					220				
Asn	Met	Gly	Tyr	Pro	Leu	Glu	Lys	His	Leu	Ala	Val	Tyr	Arg	Gln	Met
225					230					235					240
Leu	Glu	Val	Ser	Leu	Ala	Asn	Gly	Gln	Ala	Ser	Gly	Leu	Ser	Asp	Thr
				245					250					255	
Ala	Thr	Tyr	Lys	Glu	Phe	Glu	Met	Lys	Gln	Arg	Leu	Leu	Asn	Gln	Leu
			260					265					270		
Ser	Arg	Gln	Glu	Glu	Ser	Glu	Lys	Lys	Ala	Ile	Val	Leu	Ala	Ala	Asn
		275					280					285			
Tyr	Gly	Tyr	Val	Asp	Gln	Val	Leu	Thr	Thr	Ile	Lys	Ser	Ile	Cys	Tyr
	290					295					300				
His	Asn	Arg	Ser	Ile	Arg	Phe	Tyr	Leu	Ile	His	Ser	Asp	Phe	Pro	Asn
305					310					315					320
Glu	Trp	Ile	Lys	Gln	Leu	Asn	Lys	Arg	Leu	Glu	Lys	Phe	Asp	Ser	Glu
				325					330					335	

Ile Ile Asn Cys Arg Val Thr Ser Glu Gln Ile Ser Cys Tyr Lys Ser  
 340 345 350  
 Asp Ile Ser Tyr Thr Val Phe Leu Arg Tyr Phe Ile Ala Asp Phe Val  
 355 360 365  
 Gln Glu Asp Lys Ala Leu Tyr Leu Asp Cys Asp Leu Val Val Thr Lys  
 370 375 380  
 Asn Leu Asp Asp Leu Phe Ala Thr Asp Leu Gln Asp Tyr Pro Leu Ala  
 385 390 395 400  
 Ala Val Arg Asp Phe Gly Gly Arg Ala Tyr Phe Gly Gln Glu Ile Phe  
 405 410 415  
 Asn Ala Gly Val Leu Leu Val Asn Asn Ala Phe Trp Lys Lys Glu Asn  
 420 425 430  
 Met Thr Gln Lys Leu Ile Asp Val Thr Asn Glu Trp His Asp Lys Val  
 435 440 445  
 Asp Gln Ala Asp Gln Ser Ile Leu Asn Met Leu Phe Glu His Lys Trp  
 450 455 460  
 Leu Glu Leu Asp Phe Asp Tyr Asn His Ile Val Ile His Lys Gln Phe  
 465 470 475 480  
 Ala Asp Tyr Gln Leu Pro Glu Gly Gln Asp Tyr Pro Ala Ile Ile His  
 485 490 495  
 Tyr Leu Ser His Arg Lys Pro Trp Lys Asp Leu Ala Ala Gln Thr Tyr  
 500 505 510  
 Arg Glu Val Trp Trp Tyr Tyr His Gly Leu Glu Trp Thr Glu Leu Gly  
 515 520 525  
 Gln Asn His His Leu His Pro Leu Gln Arg Ser His Ile Tyr Pro Ile  
 530 535 540  
 Lys Glu Pro Phe Thr Cys Leu Ile Tyr Thr Ala Ser Asp His Ile Glu  
 545 550 555 560  
 Gln Ile Glu Thr Leu Val Gln Ser Leu Pro Asp Ile Gln Phe Lys Ile  
 565 570 575  
 Ala Ala Arg Val Ile Val Ser Asp Arg Leu Ala Gln Met Thr Ile Tyr  
 580 585 590  
 Pro Asn Val Thr Ile Phe Asn Gly Ile His Tyr Leu Val Asp Val Asp  
 595 600 605  
 Asn Glu Leu Val Glu Thr Ser Gln Val Leu Leu Asp Ile Asn His Gly  
 610 615 620  
 Glu Lys Thr Glu Glu Ile Leu Asp Gln Phe Ala Asn Leu Gly Lys Pro  
 625 630 635 640  
 Ile Leu Ser Phe Glu Asn Thr Lys Thr Tyr Glu Val Gly Gln Glu Ala  
 645 650 655  
 Tyr Ala Val Asp Gln Val Gln Ala Met Ile Glu Lys Leu Arg Glu Ile  
 660 665 670

Ser Lys

## (2) INFORMATION FOR SEQ ID NO: 201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

CATTCAGAAG CAGACCTATC AAAATCTGGA AATTATTCTT GTTGATGATG GTGCAACAGA 60  
 TGAAAGTGGT CGCTTGTGTG ATTCAATCGC TGAACAAGAT GACAGGGTGT CAGTGCCTCA 120  
 TAAAAAGAAC GAAGGATTGT CGCAAGCACG AAATGATGGG ATGAAGCAGG CTCACGGGGA 180  
 TTATCTGATT TTTATTGACT CAGATGATTA TATCCATCCA GAAATGATTC AGAGCTTATA 240  
 TGAGCAATTA GTTCAAGAAG ATGCGGATGT TTCGAGCTGT GGTGTCATGA ATGTCTATGC 300  
 TAATGATGAA AGCCACAGT CAGCCAATCA GGATGACTAT TTTGTCTGTG ATTCTCAAAC 360  
 ATTTCTAAAG GAATACCTCA TAGGTGAAAA AATACCTGGG ACGATTTGCA ATAAGCTAAT 420  
 CAAGAGACAG ATTGCAACTG CCCTATCCTT TCCTAAGGGG TTGATTTACG AAGATGCCTA 480  
 TTACCATTTT GATTTAATCA AGTTGGCCAA GAAGTATGTG GTTAATACTA AACCCTATTA 540  
 TTACTATTTT CATAGAGGGG ATAGTATTAC GACCAAACCC TATGCAGAGA AGGATTTAGC 600  
 CTATATTGAT ATCTACCAA AGTTTTATAA TGAAGTTGTG AAAAATATC CTGACTTGAA 660  
 AGAGGTCGCT TTTTTCAGAT TGGCCTATGC CCACTTCTTT ATTCTGGATA AGATGTTGCT 720  
 AGATGATCAG TATAACAGT TTGAAGCCTA TTCTCAGATT CATCGTTTTT TAAAAGGCCA 780  
 TGCCTTTGCT ATTTCTAGGA ATCCAATTTT CCGTAAGGGG AGAAGAATTA GTGCTTTGGC 840  
 CCTATTCATA AATATTTCTT TATATCGATT CTTATTACTG AAAAATATTG AAAAATCTAA 900  
 AAAATTACAT 910

## (2) INFORMATION FOR SEQ ID NO:202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ile Gln Lys Gln Thr Tyr Gln Asn Leu Glu Ile Ile Leu Val Asp Asp  
 1 5 10 15  
 Gly Ala Thr Asp Glu Ser Gly Arg Leu Cys Asp Ser Ile Ala Glu Gln

20					25					30					
Asp	Asp	Arg	Val	Ser	Val	Leu	His	Lys	Lys	Asn	Glu	Gly	Leu	Ser	Gln
		35					40					45			
Ala	Arg	Asn	Asp	Gly	Met	Lys	Gln	Ala	His	Gly	Asp	Tyr	Leu	Ile	Phe
	50					55					60				
Ile	Asp	Ser	Asp	Asp	Tyr	Ile	His	Pro	Glu	Met	Ile	Gln	Ser	Leu	Tyr
65					70					75					80
Glu	Gln	Leu	Val	Gln	Glu	Asp	Ala	Asp	Val	Ser	Ser	Cys	Gly	Val	Met
				85					90					95	
Asn	Val	Tyr	Ala	Asn	Asp	Glu	Ser	Pro	Gln	Ser	Ala	Asn	Gln	Asp	Asp
			100					105					110		
Tyr	Phe	Val	Cys	Asp	Ser	Gln	Thr	Phe	Leu	Lys	Glu	Tyr	Leu	Ile	Gly
		115					120					125			
Glu	Lys	Ile	Pro	Gly	Thr	Ile	Cys	Asn	Lys	Leu	Ile	Lys	Arg	Gln	Ile
	130					135					140				
Ala	Thr	Ala	Leu	Ser	Phe	Pro	Lys	Gly	Leu	Ile	Tyr	Glu	Asp	Ala	Tyr
145					150					155					160
Tyr	His	Phe	Asp	Leu	Ile	Lys	Leu	Ala	Lys	Lys	Tyr	Val	Val	Asn	Thr
				165					170					175	
Lys	Pro	Tyr	Tyr	Tyr	Tyr	Phe	His	Arg	Gly	Asp	Ser	Ile	Thr	Thr	Lys
			180					185					190		
Pro	Tyr	Ala	Glu	Lys	Asp	Leu	Ala	Tyr	Ile	Asp	Ile	Tyr	Gln	Lys	Phe
		195				200					205				
Tyr	Asn	Glu	Val	Val	Lys	Asn	Tyr	Pro	Asp	Leu	Lys	Glu	Val	Ala	Phe
	210					215					220				
Phe	Arg	Leu	Ala	Tyr	Ala	His	Phe	Phe	Ile	Leu	Asp	Lys	Met	Leu	Leu
225					230					235					240
Asp	Asp	Gln	Tyr	Lys	Gln	Phe	Glu	Ala	Tyr	Ser	Gln	Ile	His	Arg	Phe
				245					250					255	
Leu	Lys	Gly	His	Ala	Phe	Ala	Ile	Ser	Arg	Asn	Pro	Ile	Phe	Arg	Lys
			260					265					270		
Gly	Arg	Arg	Ile	Ser	Ala	Leu	Ala	Leu	Phe	Ile	Asn	Ile	Ser	Leu	Tyr
	275					280					285				
Arg	Phe	Leu	Leu	Leu	Lys	Asn	Ile	Glu	Lys	Ser	Lys	Lys	Leu	His	
	290					295					300				

## (2) INFORMATION FOR SEQ ID NO: 203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

TAAGGCTGAT AATCGTGTTC AAATGAGAAC GACGATTAAT AATGAATCGC CATTGTTGCT 60  
 TTCTCCGTTG TATGGCAATG ATAATGGTAA CGGATTATGG TGGGGGAACA CATTGAAGGG 120  
 AGCATGGGAA GCTATTCCTG AAGATGTAAA GCCATATGCA GCGATTGAAC TTCATCCTGC 180  
 AAAAGTCTGT AAACCAACAA GTTGTATTCC ACGAGATACG AAAGAATTGA GAGAATGGTA 240  
 TGTCAAGATG TTGGAGGAAG CTCAAAGTCT AAACATTCCA GTTTTCTTGG TTATTATGTC 300  
 GGCTGGAGAG CGTAATACAG TTCCTCCAGA GTGGTTAGAT GAACAATTCC AAAAGTATAG 360  
 TGTGTTAAAA GGTGTTTTAA ATATTGAGAA TTATTGGATT TACAATAACC AGTTAGCTCC 420  
 GCATAGTGCT AAATATTTGG AAGTTTGTGC CAAATATGGA GCGCATTTTA TCTGGCATGA 480  
 TCATGAAAAA TGGTTCTGGG AAACATTAT GAATGATCCG ACATTCTTTG AAGCGAGTCA 540  
 AAAATATCAT AAAAATTTGG TGTGGCAAC TAAAAATACG CCAATAAGAG ATGATGCGGG 600  
 TACAGATTCT ATCGTTAGTG GATTTTGGTT GAGTGGCTTA TGTGATAACT GGGGCTCATC 660  
 AACAGATACA TGGAAATGGT GGGAAAAACA TTATACAAAC ACATTTGAAA CTGGAAGAGC 720  
 TAGGGATATG AGATCCTATG CATCGGAACC AGAATCAATG ATTGCTATGG AAATGATGAA 780  
 TGTATATACT GGGGGAGGCA CAGTTTATAA TTTCGAATGT GCCGCGTATA CATTTATGAC 840  
 AAATGATGTA CCAACTCCAG CATTTACTAA AGGTATTATT CCTTTCTTTA GACATGCTAT 900  
 ACAAATCCA GCTCCAAGTA AGGAAGAAGT TGTAATAGA ACAAAGCTG TATTTTGGAA 960  
 TGGAGAAGGT AGGATTAGTT CATTAAACGG ATTTTATCAA GGACTTTATT CGAATGATGA 1020  
 AACAATGCCT TTATATAATA ATGGGAGATA TCATATTCTT CCTGTAATAC ATGAGAAAAT 1080  
 TGATAAGGAA AAGATTTTAT CTATATTCCC TAATGCAAAA ATTTTGACTA AAAATAGTGA 1140  
 GGAATTGTCT AGTAAAGTCA ACTATTTAAA CTCGCTTTAT CCAAACTTT ATGAAGGAGA 1200  
 TGGGTATGCT CAGCGTGTAG GTAATTCCTG GTATATTTAT AATAGTAATG CTAATATCAA 1260  
 TAAAAATCAG CAAGTAATGT TGCCTATGTA TACTAATAAT ACAAAGTCGT TATCGTTAGA 1320  
 TTTGACGCCA CATACTTACG CTGTTGTAA AGAAAATCCA AATAATTTAC ATATTTTATT 1380  
 GAATAATTAC AGGACAGATA AGACAGCTAT GTGGGCATTA TCAGGAAATT TTGATGCATC 1440  
 AAAAAGTTGG AAGAAAGAAG AATTAGAGTT AGCGAACTGG ATAAGCAAAA ATTATTCCAT 1500  
 CAATCCTGTA GATAATGACT TTAGGACAAC AACACTTACA TTAAAAGGGC ATACTGGTCA 1560  
 TAAACCTCAG ATAAATATAA GTGGCGATAA AAATCATTAT ACTTATACAG AAAATTGGGA 1620  
 TGAGAATACC CATGTTTATA CCATTACGGT TAATCATAAT GGAATGGTAG AGATGTCTAT 1680  
 AAATACTGAG GGGACAGGTC CAGTCTCTTT CCCAACACCA GATAAATTTA ATGATGGTAA 1740  
 TTTGAATATA GCATATGCAA AACCAACAAC ACAAAGTTCT GTAGATTACA ATGGAGACCC 1800  
 TAATAGAGCT GTGGATGGTA ACAGAAATGG TAATTTTAAAC TCTGGTTCGG TAACACACAC 1860  
 TAGGGCAGAT AATCCCTCTT GGTGGGAAGT CGATTTGAAA AAAATGGATA AAGTTGGGCT 1920

TGTAAAAATT TATAATCGCA CAGATGCTGA GACTCAACGT CTATCTAATT TT

1972


## (2) INFORMATION FOR SEQ ID NO:204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:



Lys Ala Asp Asn Arg Val Gln Met Arg Thr Thr Ile Asn Asn Glu Ser  
 1 5 10 15  
 Pro Leu Leu Leu Ser Pro Leu Tyr Gly Asn Asp Asn Gly Asn Gly Leu  
 20 25 30  
 Trp Trp Gly Asn Thr Leu Lys Gly Ala Trp Glu Ala Ile Pro Glu Asp  
 35 40 45  
 Val Lys Pro Tyr Ala Ala Ile Glu Leu His Pro Ala Lys Val Cys Lys  
 50 55 60  
 Pro Thr Ser Cys Ile Pro Arg Asp Thr Lys Glu Leu Arg Glu Trp Tyr  
 65 70 75 80  
 Val Lys Met Leu Glu Glu Ala Gln Ser Leu Asn Ile Pro Val Phe Leu  
 85 90 95  
 Val Ile Met Ser Ala Gly Glu Arg Asn Thr Val Pro Pro Glu Trp Leu  
 100 105 110  
 Asp Glu Gln Phe Gln Lys Tyr Ser Val Leu Lys Gly Val Leu Asn Ile  
 115 120 125  
 Glu Asn Tyr Trp Ile Tyr Asn Asn Gln Leu Ala Pro His Ser Ala Lys  
 130 135 140  
 Tyr Leu Glu Val Cys Ala Lys Tyr Gly Ala His Phe Ile Trp His Asp  
 145 150 155 160  
 His Glu Lys Trp Phe Trp Glu Thr Ile Met Asn Asp Pro Thr Phe Phe  
 165 170 175  
 Glu Ala Ser Gln Lys Tyr His Lys Asn Leu Val Leu Ala Thr Lys Asn  
 180 185 190  
 Thr Pro Ile Arg Asp Asp Ala Gly Thr Asp Ser Ile Val Ser Gly Phe  
 195 200 205  
 Trp Leu Ser Gly Leu Cys Asp Asn Trp Gly Ser Ser Thr Asp Thr Trp  
 210 215 220  
 Lys Trp Trp Glu Lys His Tyr Thr Asn Thr Phe Glu Thr Gly Arg Ala  
 225 230 235 240  
 Arg Asp Met Arg Ser Tyr Ala Ser Glu Pro Glu Ser Met Ile Ala Met  
 245 250 255

Glu Met Met Asn Val Tyr Thr Gly Gly Gly Thr Val Tyr Asn Phe Glu  
 260 265 270  
 Cys Ala Ala Tyr Thr Phe Met Thr Asn Asp Val Pro Thr Pro Ala Phe  
 275 280 285  
 Thr Lys Gly Ile Ile Pro Phe Phe Arg His Ala Ile Gln Asn Pro Ala  
 290 295 300  
 Pro Ser Lys Glu Glu Val Val Asn Arg Thr Lys Ala Val Phe Trp Asn  
 305 310 315 320  
 Gly Glu Gly Arg Ile Ser Ser Leu Asn Gly Phe Tyr Gln Gly Leu Tyr  
 325 330 335  
 Ser Asn Asp Glu Thr Met Pro Leu Tyr Asn Asn Gly Arg Tyr His Ile  
 340 345 350  
 Leu Pro Val Ile His Glu Lys Ile Asp Lys Glu Lys Ile Ser Ser Ile  
 355 360 365  
 Phe Pro Asn Ala Lys Ile Leu Thr Lys Asn Ser Glu Glu Leu Ser Ser  
 370 375 380  
 Lys Val Asn Tyr Leu Asn Ser Leu Tyr Pro Lys Leu Tyr Glu Gly Asp  
 385 390 395 400  
 Gly Tyr Ala Gln Arg Val Gly Asn Ser Trp Tyr Ile Tyr Asn Ser Asn  
 405 410 415  
 Ala Asn Ile Asn Lys Asn Gln Gln Val Met Leu Pro Met Tyr Thr Asn  
 420 425 430  
 Asn Thr Lys Ser Leu Ser Leu Asp Leu Thr Pro His Thr Tyr Ala Val  
 435 440 445  
 Val Lys Glu Asn Pro Asn Asn Leu His Ile Leu Leu Asn Asn Tyr Arg  
 450 455 460  
 Thr Asp Lys Thr Ala Met Trp Ala Leu Ser Gly Asn Phe Asp Ala Ser  
 465 470 475 480  
 Lys Ser Trp Lys Lys Glu Glu Leu Glu Leu Ala Asn Trp Ile Ser Lys  
 485 490 495  
 Asn Tyr Ser Ile Asn Pro Val Asp Asn Asp Phe Arg Thr Thr Thr Leu  
 500 505 510  
 Thr Leu Lys Gly His Thr Gly His Lys Pro Gln Ile Asn Ile Ser Gly  
 515 520 525  
 Asp Lys Asn His Tyr Thr Tyr Thr Glu Asn Trp Asp Glu Asn Thr His  
 530 535 540  
 Val Tyr Thr Ile Thr Val Asn His Asn Gly Met Val Glu Met Ser Ile  
 545 550 555 560  
 Asn Thr Glu Gly Thr Gly Pro Val Ser Phe Pro Thr Pro Asp Lys Phe  
 565 570 575  
 Asn Asp Gly Asn Leu Asn Ile Ala Tyr Ala Lys Pro Thr Thr Gln Ser  
 580 585 590  
 Ser Val Asp Tyr Asn Gly Asp Pro Asn Arg Ala Val Asp Gly Asn Arg



595 600 605

Asn Gly Asn Phe Asn Ser Gly Ser Val Thr His Thr Arg Ala Asp Asn  
610 615 620

Pro Ser Trp Trp Glu Val Asp Leu Lys Lys Met Asp Lys Val Gly Leu  
625 630 635 640

Val Lys Ile Tyr Asn Arg Thr Asp Ala Glu Thr Gln Arg Leu Ser Asn  
645 650 655

Phe

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

CTGTGGCAAT CAGTCAGCTG CTTCCAAACA GTCAGCTTCA GGAACGATTG AGGTGATTTC 60

ACGAGAAAAT GGCTCTGGGA CACGGGGTGC CTTACAGAGAA ATCACAGGGA TTCTCAAAAA 120

AGACGGTGAT AAAAAAATTG ACAACACTGC CAAAACAGCT GTGATTCAAA ATAGTACAGA 180

AGGTGTTCTC TCAGCAGTTC AAGGGAATGC TAATGCTATC GGCTACATCT CCTTGGGATC 240

TTTAACGAAA TCTGTCAAGG CTTTAGAGAT TGATGGTGTC AAGGCTAGTC GAGACACAGT 300

TTTAGATGGT GAATACCCTC TTCAACGTCC CTTCAACATT GTTTGGTCTT CTAATCTTTC 360

CAAGCTAGGT CAAGATTTTA TCAGCTTTAT CCACTCCAAA CAAGGTCAAC AAGTGGTCAC 420

AGATAATAAA TTTATTGAAG CTAAAACCGA AACCACGGAA TATACAAGCC AACACTTATC 480

AGGCAAGTTG TCTGTTGTAG GTTCCACTTC AGTATCTTCT TTAATGGAAA AATTAGCAGA 540

AGCTTATAAA AAAGAAAATC CAGAAGTTAC GATTGATATT ACCTCTAATG GGTCTTCAGC 600

AGGTATTACC GCTGTTAAGG AGAAAACCGC TGATATTGGT ATGGTTTCTA GGGAATTAAAC 660

TCCTGAAGAA GGTAAGAGTC TCACCCATGA TGCTATTGCT TTAGACGGTA TTGCTGTTGT 720

GGTCAATAAT GACAATAAGG CAAGCCAAGT CAGTATGGCT GAACTTGCAG ACGTTTTTAG 780

TGGCAAATTA ACCACCTGGG ACAAGATTAA A 811


(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:



Cys Gly Asn Gln Ser Ala Ala Ser Lys Gln Ser Ala Ser Gly Thr Ile  
 1 5 10 15  
 Glu Val Ile Ser Arg Glu Asn Gly Ser Gly Thr Arg Gly Ala Phe Thr  
 20 25 30  
 Glu Ile Thr Gly Ile Leu Lys Lys Asp Gly Asp Lys Lys Ile Asp Asn  
 35 40 45  
 Thr Ala Lys Thr Ala Val Ile Gln Asn Ser Thr Glu Gly Val Leu Ser  
 50 55 60  
 Ala Val Gln Gly Asn Ala Asn Ala Ile Gly Tyr Ile Ser Leu Gly Ser  
 65 70 75 80  
 Leu Thr Lys Ser Val Lys Ala Leu Glu Ile Asp Gly Val Lys Ala Ser  
 85 90 95  
 Arg Asp Thr Val Leu Asp Gly Glu Tyr Pro Leu Gln Arg Pro Phe Asn  
 100 105 110  
 Ile Val Trp Ser Ser Asn Leu Ser Lys Leu Gly Gln Asp Phe Ile Ser  
 115 120 125  
 Phe Ile His Ser Lys Gln Gly Gln Gln Val Val Thr Asp Asn Lys Phe  
 130 135 140  
 Ile Glu Ala Lys Thr Glu Thr Thr Glu Tyr Thr Ser Gln His Leu Ser  
 145 150 155 160  
 Gly Lys Leu Ser Val Val Gly Ser Thr Ser Val Ser Ser Leu Met Glu  
 165 170 175  
 Lys Leu Ala Glu Ala Tyr Lys Lys Glu Asn Pro Glu Val Thr Ile Asp  
 180 185 190  
 Ile Thr Ser Asn Gly Ser Ser Ala Gly Ile Thr Ala Val Lys Glu Lys  
 195 200 205  
 Thr Ala Asp Ile Gly Met Val Ser Arg Glu Leu Thr Pro Glu Glu Gly  
 210 215 220  
 Lys Ser Leu Thr His Asp Ala Ile Ala Leu Asp Gly Ile Ala Val Val  
 225 230 235 240  
 Val Asn Asn Asp Asn Lys Ala Ser Gln Val Ser Met Ala Glu Leu Ala  
 245 250 255  
 Asp Val Phe Ser Gly Lys Leu Thr Thr Trp Asp Lys Ile Lys  
 260 265 270

## (2) INFORMATION FOR SEQ ID NO: 207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

TTGTCAACAA CAACATGCTA CTTCTGAGGG GACGAATCAA AGGCAAAGCA GTTCAGCGAA 60  
 AGTTCCATGG AAAGCTTCAT ACACCAACCT AAACAACCAG GTAAGTACAG AAGAGGTCAA 120  
 ATCTCTCTTA TCAGCTCACT TGGATCCAAA TAGTGTTGAT GCATTTTTTA ATCTCGTTAA 180  
 TGACTATAAT ACCATTGTCG GCTCAACTGG CTTATCAGGA GATTTCACTT CCTTTACTCA 240  
 CACCGAATAC GATGTTGAGA AAATCAGTCA TCTCTGGAAT CAAAAGAAGG GCGATTTTGT 300  
 TGGGACCAAC TGCCGTATCA ATAGTTATTG TCTTTTGAAA AATTCAGTCA CCATTCCAAA 360  
 GCTTGAAAAG AATGACCAGT TGCTTTTCCT AGATAATGAT GCGATTGATA AAGGAAAGGT 420  
 CTTTGATTCA CAAGATAAGG AAGAGTTTGA TATTCTATTT TCGAGAGTTC CAACTGAGTC 480  
 AACTACAGAT GTCAAGGTTT ACGCTGAAAA GATGGAAGCA TTCTTCTCAC AATTTCAATT 540  
 CAATGAAAAA GCTCGAATGC TGTCTGTAGT CTTGCACGAC AATTTGGATG GCGAGTATCT 600  
 GTTTGTAGGC CACGTTGGGG TCTTAGTACC TGCTGATGAC GGTTCCTTAT TTGTAGAGAA 660  
 ATTGACTTTC GAAGAGCCCT ACCAAGCGAT TAAATTTGCT AGTAAGGAAG ATTGCTACAA 720  
 GTATTTGGGC ACCAAGTATG CGGATTATAC AGGCGAGGGA CTGGCTAAGC CTTTTATCAT 780  
 GGATAATGAT AAGTGGGTTA AACTT 805

## (2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 268 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Cys Gln Gln Gln His Ala Thr Ser Glu Gly Thr Asn Gln Arg Gln Ser  
 1 5 10 15  
 Ser Ser Ala Lys Val Pro Trp Lys Ala Ser Tyr Thr Asn Leu Asn Asn  
 20 25 30  
 Gln Val Ser Thr Glu Glu Val Lys Ser Leu Leu Ser Ala His Leu Asp  
 35 40 45  
 Pro Asn Ser Val Asp Ala Phe Phe Asn Leu Val Asn Asp Tyr Asn Thr  
 50 55 60  
 Ile Val Gly Ser Thr Gly Leu Ser Gly Asp Phe Thr Ser Phe Thr His  
 65 70 75 80  
 Thr Glu Tyr Asp Val Glu Lys Ile Ser His Leu Trp Asn Gln Lys Lys  
 85 90 95  
 Gly Asp Phe Val Gly Thr Asn Cys Arg Ile Asn Ser Tyr Cys Leu Leu  
 100 105 110

Lys Asn Ser Val Thr Ile Pro Lys Leu Glu Lys Asn Asp Gln Leu Leu  
 115 120 125  
 Phe Leu Asp Asn Asp Ala Ile Asp Lys Gly Lys Val Phe Asp Ser Gln  
 130 135 140  
 Asp Lys Glu Glu Phe Asp Ile Leu Phe Ser Arg Val Pro Thr Glu Ser  
 145 150 155 160  
 Thr Thr Asp Val Lys Val His Ala Glu Lys Met Glu Ala Phe Phe Ser  
 165 170 175  
 Gln Phe Gln Phe Asn Glu Lys Ala Arg Met Leu Ser Val Val Leu His  
 180 185 190  
 Asp Asn Leu Asp Gly Glu Tyr Leu Phe Val Gly His Val Gly Val Leu  
 195 200 205  
 Val Pro Ala Asp Asp Gly Phe Leu Phe Val Glu Lys Leu Thr Phe Glu  
 210 215 220  
 Glu Pro Tyr Gln Ala Ile Lys Phe Ala Ser Lys Glu Asp Cys Tyr Lys  
 225 230 235 240  
 Tyr Leu Gly Thr Lys Tyr Ala Asp Tyr Thr Gly Glu Gly Leu Ala Lys  
 245 250 255  
 Pro Phe Ile Met Asp Asn Asp Lys Trp Val Lys Leu  
 260 265

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TTGTTTCAGGC AAGTCCGTGA CTAGTGAACA CCAAACGAAA GATGAAATGA AGACGGAGCA	60
GACAGCTAGT AAAACAAGCG CAGCTAAAGG GAAAGAGGTG GCTGATTTTG AATTGATGGG	120
AGTAGATGGC AAGACCTACC GTTTATCTGA TTACAAGGGC AAGAAAGTCT ATCTCAAATT	180
CTGGGCTTCT TGGTGTTCCTA TCTGTCTGGC TAGTCTTCCA GATACGGATG AGATTGCTAA	240
AGAAGCTGGT GATGACTATG TGGTCTTGAC AGTAGTGTCA CCAGGACATA AGGGAGAGCA	300
ATCTGAAGCG GACTTTAAGA ATTGGTATAA GGGATTGGAT TATAAAAATC TCCCAGTCCT	360
AGTTGACCCA TCAGGCAAAC TTTTGGAAAC TTATGGTGTC CGTTCCTTACC CAACCCAAGC	420
CTTTATAGAC AAAGAAGGCA AGCTGGTCAA AACACATCCA GGATTCATGG AAAAAGATGC	480
AATTTTGCAA ACTTTGAAGG AATTAGCC	508

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Cys Ser Gly Lys Ser Val Thr Ser Glu His Gln Thr Lys Asp Glu Met  
 1 5 10 15  
 Lys Thr Glu Gln Thr Ala Ser Lys Thr Ser Ala Ala Lys Gly Lys Glu  
 20 25 30  
 Val Ala Asp Phe Glu Leu Met Gly Val Asp Gly Lys Thr Tyr Arg Leu  
 35 40 45  
 Ser Asp Tyr Lys Gly Lys Lys Val Tyr Leu Lys Phe Trp Ala Ser Trp  
 50 55 60  
 Cys Ser Ile Cys Leu Ala Ser Leu Pro Asp Thr Asp Glu Ile Ala Lys  
 65 70 75 80  
 Glu Ala Gly Asp Asp Tyr Val Val Leu Thr Val Val Ser Pro Gly His  
 85 90 95  
 Lys Gly Glu Gln Ser Glu Ala Asp Phe Lys Asn Trp Tyr Lys Gly Leu  
 100 105 110  
 Asp Tyr Lys Asn Leu Pro Val Leu Val Asp Pro Ser Gly Lys Leu Leu  
 115 120 125  
 Glu Thr Tyr Gly Val Arg Ser Tyr Pro Thr Gln Ala Phe Ile Asp Lys  
 130 135 140  
 Glu Gly Lys Leu Val Lys Thr His Pro Gly Phe Met Glu Lys Asp Ala  
 145 150 155 160  
 Ile Leu Gln Thr Leu Lys Glu Leu Ala  
 165

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 994 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CTCGCAAATT GAAAAGGCGG CAGTTAGCCA AGGAGGAAAA GCAGTGAAAA AACAGAAAT 60  
 TAGTAAAGAC GCAGACTTGC ACGAAATTTA TCTAGCTGGA GGTGTGTTCT GGGGAGTGGA 120  
 GGAATATTTT TCACGTGTTT CCGGGGTGAC GGATGCCGTT TCAGGCTATG CAAATGGTAG 180  
 AGGAGAAACA ACCAAGTACG AATTGATTAA CCAAACAGGT CATGCAGAAA CCGTCCATGT 240  
 CACCTATGAT GCCAAGCAAA TTTCTCTCAA GGAAATCCTG CTTCACTATT TCCGCATTAT 300

CAATCCAACC AGCAAAAATA AACAAGGAAA TGATGTGGGG ACCCAGTACC GTACTGGTGT 360  
 TTATTACACA GATGACAAGG ATTTGGAAGT GATTAACCAA GTCTTTGATG AGGTGGCTAA 420  
 GAAATACGAT CAACCTCTAG CAGTTGAAAA GGAAAACCTTG AAGAATTTTG TGGTGGCTGA 480  
 GGATTACCAT CAAGACTATC TCAAGAAAAA TCCAAATGGC TACTGCCATA TCAATGTAA 540  
 TCAGGCGGCC TATCCTGTCA TTGATGCCAG CAAATATCCA AAACCAAGTG ATGAGGAATT 600  
 GAAAAAGACC CTGTCACCTG AGGAGTATGC AGTTACCCAG GAAAATCAAA CAGAACGAGC 660  
 TTTCTCAAAC CGTTACTGGG ATAAATTTGA ATCCGGTATC TATGTGGATA TAGCAACTGG 720  
 GGAACCTCTC TTTTCATCAA AAGACAAATT TGAGTCTGGT TGTGGCTGGC CTAGTTTAC 780  
 CCAACCCATC AGTCCAGATG TTGTCACCTA CAAGGAAGAT AAGTCCTACA ATATGACGCG 840  
 TATGGAAGTG CGGAGCCGAG TAGGAGATTC TCACCTTGGG CATGTCTTTA CGGATGGTCC 900  
 ACAGGACAAG GCGGGCTTAC GTTACTGTAT CAATAGCCTC TCTATCCGCT TTATCCCAA 960  
 AGACCAAATG GAAGAAAAAG GTACGCTTAT TTAC 994

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ser Gln Ile Glu Lys Ala Ala Val Ser Gln Gly Gly Lys Ala Val Lys  
 1 5 10 15  
 Lys Thr Glu Ile Ser Lys Asp Ala Asp Leu His Glu Ile Tyr Leu Ala  
 20 25 30  
 Gly Gly Cys Phe Trp Gly Val Glu Glu Tyr Phe Ser Arg Val Pro Gly  
 35 40 45  
 Val Thr Asp Ala Val Ser Gly Tyr Ala Asn Gly Arg Gly Glu Thr Thr  
 50 55 60  
 Lys Tyr Glu Leu Ile Asn Gln Thr Gly His Ala Glu Thr Val His Val  
 65 70 75 80  
 Thr Tyr Asp Ala Lys Gln Ile Ser Leu Lys Glu Ile Leu Leu His Tyr  
 85 90 95  
 Phe Arg Ile Ile Asn Pro Thr Ser Lys Asn Lys Gln Gly Asn Asp Val  
 100 105 110  
 Gly Thr Gln Tyr Arg Thr Gly Val Tyr Tyr Thr Asp Asp Lys Asp Leu  
 115 120 125  
 Glu Val Ile Asn Gln Val Phe Asp Glu Val Ala Lys Lys Tyr Asp Gln  
 130 135 140

Pro Leu Ala Val Glu Lys Glu Asn Leu Lys Asn Phe Val Val Ala Glu  
 145 150 155 160  
 Asp Tyr His Gln Asp Tyr Leu Lys Lys Asn Pro Asn Gly Tyr Cys His  
 165 170 175  
 Ile Asn Val Asn Gln Ala Ala Tyr Pro Val Ile Asp Ala Ser Lys Tyr  
 180 185 190  
 Pro Lys Pro Ser Asp Glu Glu Leu Lys Lys Thr Leu Ser Pro Glu Glu  
 195 200 205  
 Tyr Ala Val Thr Gln Glu Asn Gln Thr Glu Arg Ala Phe Ser Asn Arg  
 210 215 220  
 Tyr Trp Asp Lys Phe Glu Ser Gly Ile Tyr Val Asp Ile Ala Thr Gly  
 225 230 235 240  
 Glu Pro Leu Phe Ser Ser Lys Asp Lys Phe Glu Ser Gly Cys Gly Trp  
 245 250 255  
 Pro Ser Phe Thr Gln Pro Ile Ser Pro Asp Val Val Thr Tyr Lys Glu  
 260 265 270  
 Asp Lys Ser Tyr Asn Met Thr Arg Met Glu Val Arg Ser Arg Val Gly  
 275 280 285  
 Asp Ser His Leu Gly His Val Phe Thr Asp Gly Pro Gln Asp Lys Gly  
 290 295 300  
 Gly Leu Arg Tyr Cys Ile Asn Ser Leu Ser Ile Arg Phe Ile Pro Lys  
 305 310 315 320  
 Asp Gln Met Glu Glu Lys Gly Thr Leu Ile Tyr  
 325 330

## (2) INFORMATION FOR SEQ ID NO: 213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TTGTCAGTCA GGTCTAATG GTTCTCAGTC TGCTGTGGAT GCTATCAAAC AAAAAGGGAA	60
ATTAGTTGTG GCAACCAGTC CTGACTATGC ACCCTTTGAA TTTCAATCAT TGGTTGATGG	120
AAAGAACCAG GTAGTCGGTG CAGACATCGA CATGGCTCAG GCTATCGCTG ATGAAC TTGG	180
GGTTAAGTTG GAAATCTCAA GCATGAGTTT TGACAATGTT TTGACCAGTC TTCAA ACTGG	240
TAAGGCTGAC CTAGCAGTTG CAGGAATTAG TGCTACTGAC GAGAGAAAAG AAGTCTTTGA	300
TTTTTCAATC CCATACTATG AAAACAAGAT TAGTTTCTTG GTTCGTAAGG CTGATGTGGA	360
AAAATACAAG GATTTAAC TA GCCTAGAAAAG TGCTAATATT GCAGCCCAA AAGGGACTGT	420
TCCAGAATCA ATGGTCAAGG AACAA TTGCC AAAAGTTCAA TTAAC TTCCC TAACTAATAT	480

GGGTGAAGCA GTCAATGAAT TGCAGGCTGG AAAAATAGAT GCTGTTTCATA TGGATGAGCC 540  
 TGTTCACCTT AGTTATGCTG CTAAAAACGC TGGCTTAGCT GTCGCAACTG TCAGCTTGAA 600  
 GATGAAGGAC GGCGACGCCA ATGCC 625

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Cys Gln Ser Gly Ser Asn Gly Ser Gln Ser Ala Val Asp Ala Ile Lys  
 1 5 10 15  
 Gln Lys Gly Lys Leu Val Val Ala Thr Ser Pro Asp Tyr Ala Pro Phe  
 20 25 30  
 Glu Phe Gln Ser Leu Val Asp Gly Lys Asn Gln Val Val Gly Ala Asp  
 35 40 45  
 Ile Asp Met Ala Gln Ala Ile Ala Asp Glu Leu Gly Val Lys Leu Glu  
 50 55 60  
 Ile Ser Ser Met Ser Phe Asp Asn Val Leu Thr Ser Leu Gln Thr Gly  
 65 70 75 80  
 Lys Ala Asp Leu Ala Val Ala Gly Ile Ser Ala Thr Asp Glu Arg Lys  
 85 90 95  
 Glu Val Phe Asp Phe Ser Ile Pro Tyr Tyr Glu Asn Lys Ile Ser Phe  
 100 105 110  
 Leu Val Arg Lys Ala Asp Val Glu Lys Tyr Lys Asp Leu Thr Ser Leu  
 115 120 125  
 Glu Ser Ala Asn Ile Ala Ala Gln Lys Gly Thr Val Pro Glu Ser Met  
 130 135 140  
 Val Lys Glu Gln Leu Pro Lys Val Gln Leu Thr Ser Leu Thr Asn Met  
 145 150 155 160  
 Gly Glu Ala Val Asn Glu Leu Gln Ala Gly Lys Ile Asp Ala Val His  
 165 170 175  
 Met Asp Glu Pro Val Ala Leu Ser Tyr Ala Ala Lys Asn Ala Gly Leu  
 180 185 190  
 Ala Val Ala Thr Val Ser Leu Lys Met Lys Asp Gly Asp Ala Asn Ala  
 195 200 205


(2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3022 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:



GGAAACTTCA CAGGATTTTA AAGAGAAGAA AACAGCAGTC ATTAAGGAAA AAGAAGTTGT	60
TAGTAAAAAT CCTGTGATAG ACAATAACAC TAGCAATGAA GAAGCAAAAA TCAAAGAAGA	120
AAATTCCAAT AAATCCCAAG GAGATTATAC GGACTCATTT GTGAATAAAA ACACAGAAAA	180
TCCCCAAAAA GAAGATAAAG TTGTCTATAT TGCTGAATTT AAAGATAAAG AATCTGGAGA	240
AAAAGCAATC AAGGAACAT CCAGTCTTAA GAATACAAAA GTTTTATATA CTTATGATAG	300
AATTTTAAAC GGTAGTGCCA TAGAAACAAC TCCAGATAAC TTGGACAAAA TTAAACAAAT	360
AGAAGGTATT TCATCGGTTG AAAGGGCACA AAAAGTCCAA CCCATGATGA ATCATGCCAG	420
AAAGGAAATT GGAGTTGAGG AAGCTATTGA TTACCTAAAG TCTATCAATG CTCCGTTTGG	480
GAAAAATTTT GATGGTAGAG GTATGGTCAT TTCAAATATC GATACTGGAA CAGATTATAG	540
ACATAAGGCT ATGAGAATCG ATGATGATGC CAAAGCCTCA ATGAGATTTA AAAAAGAAGA	600
CTTAAAAGGC ACTGATAAAA ATTATTGGTT GAGTGATAAA ATCCCTCATG CGTTCAATTA	660
TTATAATGGT GGCAAAATCA CTGTAGAAAA ATATGATGAT GGAAGGGATT ATTTTGACCC	720
ACATGGGATG CATATTGCAG GGATTCTTGC TGGAAATGAT ACTGAACAAG ACATCAAAAA	780
CTTTAACGGC ATAGATGGAA TTGCACCTAA TGCACAAATT TTCTCTTACA AAATGTATTTC	840
TGACGCAGGA TCTGGGTTTG CGGGTGATGA AACAATGTTT CATGCTATTG AAGATTCTAT	900
CAAACACAAC GTTGATGTTG TTTCGGTATC ATCTGGTTTT ACAGGAACAG GTC TTGTAGG	960
TGAGAAATAT TGGCAAGCTA TTCGGGCATT AAGAAAAGCA GGCATTCCAA TGGTTGTCGC	1020
TACGGGTAAC TATGCGACTT CTGCTTCAAG TTCTTCATGG GATTTAGTAG CAAATAATCA	1080
TCTGAAAATG ACCGACACTG GAAATGTAAC ACGAACTGCA GCACATGAAG ATGCGATAGC	1140
GGTCGCTTCT GCTAAAAATC AAACAGTTGA GTTTGATAAA GTTAACATAG GTGGAGAAAG	1200
TTTTAAATAC AGAAATATAG GGGCCTTTTT CGATAAGAGT AAAATCACAA CAAATGAAGA	1260
TGGAACAAAA GC'TCC'TAGTA AATTAAAAAT TGTATATATA GGCAAGGGGC AAGACCAAGA	1320
TTTGATAGGT TTGGATCTTA GGGGCAAAAT TGCAGTAATG GATAGAATTT ATACAAAGGA	1380
TTTAAAAAAT GCTTTTAAAA AAGCTATGGA TAAGGGTGCA CGCGCCATTA TGGTTGTAAA	1440
TACTGTAAAT TACTACAATA GAGATAATTG GACAGAGCTT CCAGCTATGG GATATGAAGC	1500
GGATGAAGGT ACTAAAAGTC AAGTGTTTTT AATTTTCAGGA GATGATGGTG TAAAGCTATG	1560
GAACATGATT AATCCTGATA AAAAACTGA AGTCAAAAGA AATAATAAAG AAGATTTTAA	1620
AGATAAATTG GAGCAATACT ATCCAATTGA TATGGAAAGT TTTAATTCCA ACAAACCGAA	1680
TGTAGGTGAC GAAAAAGAGA TTGACTTTAA GTTTGCACCT GACACAGACA AAGAACTCTA	1740

TAAAGAAGAT ATCATCGTTC CAGCAGGATC TACATCTTGG GGGCCAAGAA TAGATTTACT 1800  
 TTTAAAACCC GATGTTTCAG CACCTGGTAA AAATATTAAA TCCACGCTTA ATGTTATTAA 1860  
 TGGCAAATCA ACTTATGGCT ATATGTCAGG AACTAGTATG GCGACTCCAA TCGTGGCAGC 1920  
 TTCTACTGTT TTGATTAGAC CGAAATTAAA GGAAATGCTT GAAAGACCTG TATTGAAAAA 1980  
 TCTTAAGGGA GATGACAAAA TAGATCTTAC AAGTCTTACA AAAATTGCCC TACAAAATAC 2040  
 TGCGCGACCT ATGATGGATG CAACTTCTTG GAAAGAAAAA AGTCAATACT TTGCATCACC 2100  
 TAGACAACAG GGAGCAGGCC TAATTAATGT GGCCAATGCT TTGAGAAATG AAGTTGTAGC 2160  
 AACTTTCAAA AACACTGATT CTAAAGGTTT GGTAAGTCA TATGGTTCCA TTTCTCTTAA 2220  
 AGAAATAAAA GGTGATAAAA AATACTTTAC AATCAAGCTT CACAATACAT CAAACAGACC 2280  
 TTTGACTTTT AAAGTTTCAG CATCAGCGAT AACTACAGAT TCTCTAACTG ACAGATTAAA 2340  
 ACTTGATGAA ACATATAAAG ATGAAAAATC TCCAGATGGT AAGCAAATTG TTCCAGAAAT 2400  
 TCACCCAGAA AAAGTCAAAG GAGCAAATAT CACATTTGAG CATGATACTT TCACATAGG 2460  
 CGCAAATTC T AGCTTTGATT TGAATGCGGT TATAAATGTT GGAGAGGCCA AAAACAAAAA 2520  
 TAAATTTGTA GAATCATTTA TTCATTTTGA GTCAGTGGAA GCGATGGAAG CTCTAAACTC 2580  
 CAGCGGGAAG AAAATAAACT TCCAACCTTC TTTGTCGATG CCTCTAATGG GATTTGCTGG 2640  
 GAATTGGAAC CACGAACCAA TCCTTGATAA ATGGGCTTGG GAAGAAGGGT CAAGATCAAA 2700  
 AACACTGGGA GGTATGATG ATGATGGTAA ACCGAAAATT CCAGGAACCT TAAATAAGGG 2760  
 AATTGGTGGA GAACATGGTA TAGATAAATT TAATCCAGCA GGAGTTATAC AAAATAGAAA 2820  
 AGATAAAAAT ACAACATCCC TGGATCAAAA TCCAGAATTA TTTGCTTTCA ATAACGAAGG 2880  
 GATCAACGCT CCATCATCAA GTGGTTCTAA GATTGCTAAC ATTTATCCTT TAGATTCAAA 2940  
 TGGAAATCCT CAAGATGCTC AACTTGAAAG AGGATTAACA CCTTCTCCAC TTGTATTAAG 3000  
 AAGTGCAGAA GAAGGATTGA TT 3022

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Glu Thr Ser Gln Asp Phe Lys Glu Lys Lys Thr Ala Val Ile Lys Glu  
 1 5 10 15  
 Lys Glu Val Val Ser Lys Asn Pro Val Ile Asp Asn Asn Thr Ser Asn  
 20 25 30  
 Glu Glu Ala Lys Ile Lys Glu Glu Asn Ser Asn Lys Ser Gln Gly Asp

35 40 45  
 Tyr Thr Asp Ser Phe Val Asn Lys Asn Thr Glu Asn Pro Lys Lys Glu  
 50 55 60  
 Asp Lys Val Val Tyr Ile Ala Glu Phe Lys Asp Lys Glu Ser Gly Glu  
 65 70 75 80  
 Lys Ala Ile Lys Glu Leu Ser Ser Leu Lys Asn Thr Lys Val Leu Tyr  
 85 90 95  
 Thr Tyr Asp Arg Ile Phe Asn Gly Ser Ala Ile Glu Thr Thr Pro Asp  
 100 105 110  
 Asn Leu Asp Lys Ile Lys Gln Ile Glu Gly Ile Ser Ser Val Glu Arg  
 115 120 125  
 Ala Gln Lys Val Gln Pro Met Met Asn His Ala Arg Lys Glu Ile Gly  
 130 135 140  
 Val Glu Glu Ala Ile Asp Tyr Leu Lys Ser Ile Asn Ala Pro Phe Gly  
 145 150 155 160  
 Lys Asn Phe Asp Gly Arg Gly Met Val Ile Ser Asn Ile Asp Thr Gly  
 165 170 175  
 Thr Asp Tyr Arg His Lys Ala Met Arg Ile Asp Asp Asp Ala Lys Ala  
 180 185 190  
 Ser Met Arg Phe Lys Lys Glu Asp Leu Lys Gly Thr Asp Lys Asn Tyr  
 195 200 205  
 Trp Leu Ser Asp Lys Ile Pro His Ala Phe Asn Tyr Tyr Asn Gly Gly  
 210 215 220  
 Lys Ile Thr Val Glu Lys Tyr Asp Asp Gly Arg Asp Tyr Phe Asp Pro  
 225 230 235 240  
 His Gly Met His Ile Ala Gly Ile Leu Ala Gly Asn Asp Thr Glu Gln  
 245 250 255  
 Asp Ile Lys Asn Phe Asn Gly Ile Asp Gly Ile Ala Pro Asn Ala Gln  
 260 265 270  
 Ile Phe Ser Tyr Lys Met Tyr Ser Asp Ala Gly Ser Gly Phe Ala Gly  
 275 280 285  
 Asp Glu Thr Met Phe His Ala Ile Glu Asp Ser Ile Lys His Asn Val  
 290 295 300  
 Asp Val Val Ser Val Ser Ser Gly Phe Thr Gly Thr Gly Leu Val Gly  
 305 310 315 320  
 Glu Lys Tyr Trp Gln Ala Ile Arg Ala Leu Arg Lys Ala Gly Ile Pro  
 325 330 335  
 Met Val Val Ala Thr Gly Asn Tyr Ala Thr Ser Ala Ser Ser Ser  
 340 345 350  
 Trp Asp Leu Val Ala Asn Asn His Leu Lys Met Thr Asp Thr Gly Asn  
 355 360 365  
 Val Thr Arg Thr Ala Ala His Glu Asp Ala Ile Ala Val Ala Ser Ala  
 370 375 380

Lys Asn Gln Thr Val Glu Phe Asp Lys Val Asn Ile Gly Gly Glu Ser  
 385 390 395 400  
 Phe Lys Tyr Arg Asn Ile Gly Ala Phe Phe Asp Lys Ser Lys Ile Thr  
 405 410 415  
 Thr Asn Glu Asp Gly Thr Lys Ala Pro Ser Lys Leu Lys Phe Val Tyr  
 420 425 430  
 Ile Gly Lys Gly Gln Asp Gln Asp Leu Ile Gly Leu Asp Leu Arg Gly  
 435 440 445  
 Lys Ile Ala Val Met Asp Arg Ile Tyr Thr Lys Asp Leu Lys Asn Ala  
 450 455 460  
 Phe Lys Lys Ala Met Asp Lys Gly Ala Arg Ala Ile Met Val Val Asn  
 465 470 475 480  
 Thr Val Asn Tyr Tyr Asn Arg Asp Asn Trp Thr Glu Leu Pro Ala Met  
 485 490 495  
 Gly Tyr Glu Ala Asp Glu Gly Thr Lys Ser Gln Val Phe Ser Ile Ser  
 500 505 510  
 Gly Asp Asp Gly Val Lys Leu Trp Asn Met Ile Asn Pro Asp Lys Lys  
 515 520 525  
 Thr Glu Val Lys Arg Asn Asn Lys Glu Asp Phe Lys Asp Lys Leu Glu  
 530 535 540  
 Gln Tyr Tyr Pro Ile Asp Met Glu Ser Phe Asn Ser Asn Lys Pro Asn  
 545 550 555 560  
 Val Gly Asp Glu Lys Glu Ile Asp Phe Lys Phe Ala Pro Asp Thr Asp  
 565 570 575  
 Lys Glu Leu Tyr Lys Glu Asp Ile Ile Val Pro Ala Gly Ser Thr Ser  
 580 585 590  
 Trp Gly Pro Arg Ile Asp Leu Leu Leu Lys Pro Asp Val Ser Ala Pro  
 595 600 605  
 Gly Lys Asn Ile Lys Ser Thr Leu Asn Val Ile Asn Gly Lys Ser Thr  
 610 615 620  
 Tyr Gly Tyr Met Ser Gly Thr Ser Met Ala Thr Pro Ile Val Ala Ala  
 625 630 635 640  
 Ser Thr Val Leu Ile Arg Pro Lys Leu Lys Glu Met Leu Glu Arg Pro  
 645 650 655  
 Val Leu Lys Asn Leu Lys Gly Asp Asp Lys Ile Asp Leu Thr Ser Leu  
 660 665 670  
 Thr Lys Ile Ala Leu Gln Asn Thr Ala Arg Pro Met Met Asp Ala Thr  
 675 680 685  
 Ser Trp Lys Glu Lys Ser Gln Tyr Phe Ala Ser Pro Arg Gln Gln Gly  
 690 695 700  
 Ala Gly Leu Ile Asn Val Ala Asn Ala Leu Arg Asn Glu Val Val Ala  
 705 710 715 720


Thr Phe Lys Asn Thr Asp Ser Lys Gly Leu Val Asn Ser Tyr Gly Ser  
 725 730 735  
 Ile Ser Leu Lys Glu Ile Lys Gly Asp Lys Lys Tyr Phe Thr Ile Lys  
 740 745 750  
 Leu His Asn Thr Ser Asn Arg Pro Leu Thr Phe Lys Val Ser Ala Ser  
 755 760 765  
 Ala Ile Thr Thr Asp Ser Leu Thr Asp Arg Leu Lys Leu Asp Glu Thr  
 770 775 780  
 Tyr Lys Asp Glu Lys Ser Pro Asp Gly Lys Gln Ile Val Pro Glu Ile  
 785 790 795 800  
 His Pro Glu Lys Val Lys Gly Ala Asn Ile Thr Phe Glu His Asp Thr  
 805 810 815  
 Phe Thr Ile Gly Ala Asn Ser Ser Phe Asp Leu Asn Ala Val Ile Asn  
 820 825 830  
 Val Gly Glu Ala Lys Asn Lys Asn Lys Phe Val Glu Ser Phe Ile His  
 835 840 845  
 Phe Glu Ser Val Glu Ala Met Glu Ala Leu Asn Ser Ser Gly Lys Lys  
 850 855 860  
 Ile Asn Phe Gln Pro Ser Leu Ser Met Pro Leu Met Gly Phe Ala Gly  
 865 870 875 880  
 Asn Trp Asn His Glu Pro Ile Leu Asp Lys Trp Ala Trp Glu Glu Gly  
 885 890 895  
 Ser Arg Ser Lys Thr Leu Gly Gly Tyr Asp Asp Asp Gly Lys Pro Lys  
 900 905 910  
 Ile Pro Gly Thr Leu Asn Lys Gly Ile Gly Gly Glu His Gly Ile Asp  
 915 920 925  
 Lys Phe Asn Pro Ala Gly Val Ile Gln Asn Arg Lys Asp Lys Asn Thr  
 930 935 940  
 Thr Ser Leu Asp Gln Asn Pro Glu Leu Phe Ala Phe Asn Asn Glu Gly  
 945 950 955 960  
 Ile Asn Ala Pro Ser Ser Ser Gly Ser Lys Ile Ala Asn Ile Tyr Pro  
 965 970 975  
 Leu Asp Ser Asn Gly Asn Pro Gln Asp Ala Gln Leu Glu Arg Gly Leu  
 980 985 990  
 Thr Pro Ser Pro Leu Val Leu Arg Ser Ala Glu Glu Gly Leu Ile  
 995 1000 1005

## (2) INFORMATION FOR SEQ ID NO: 217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:



TGTGGTCGAA GTTGAGACTC CTCAATCAAT AACAAATCAG GAGCAAGCTA GGACAGAAAA	60
CCAAGTAGTA GAGACAGAGG AAGCTCCAAA AGAAGAAGCA CCTAAAACAG AAGAAAGTCC	120
AAAGGAAGAA CCAAAATCGG AGGTAAAACC TACTGACGAC ACCCTTCCTA AAGTAGAAGA	180
GGGGAAAGAA GATTCAGCAG AACCAGCTCC AGTTGAAGAA GTAGGTGGAG AAGTTGAGTC	240
AAAACCAGAG GAAAAAGTAG CAGTTAAGCC AGAAAGTCAA CCATCAGACA AACCAGCTGA	300
GGAATCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AAAAGGCACC	360
AGTCGAGCCA GAAAAGCAAC CAGAAGCTCC TGAAGAAGAG AAGGCTGTAG AGGAAACACC	420
GAAACAAGAA GAGTCAACTC CAGATACCAA GGCTGAAGAA ACTGTAGAAC CAAAAGAGGA	480
GACTGTTAAT CAATCTATTG AACAACCAAA AGTTGAAACG CCTGCTGTAG AAAAACAAAC	540
AGAACCAACA GAGGAACCAA AAGTTGAACA AGCAGGTGAA CCAGTCGCGC CAAGAGAAGA	600
CGAACAGGCA CCAACGGCAC CAGTTGAGCC AGAAAAGCAA CCAGAAGTTC CTGAAGAAGA	660
GAAGGCTGTA GAGGAAACAC CGAAACCAGA AGATAAAATA AAGGGTATTG GTACTAAAGA	720
ACCAGTTGAT AAAAGTGAGT TAAATAATCA AATTGATAAA GCTAGTTCAG TTTCTCCTAC	780
TGATTATTCT ACAGCAAGTT ACAATGCTCT TGGACCTGTT TTAGAAACTG CAAAAGGTGT	840
CTATGCTTCA GAGCCTGTAA AACAGCCTGA GGTAATAGC GAGACAAATA AACTTAAAC	900
GGCTATTGAC GCTCTAAACG TTGATAAAAC TGAATTAAAC AATACGATTG CAGATGCAAA	960
AACAAAGGTA AAAGAACATT ACAGTGATAG AAGTTGGCAA AACCTCCAAA CTGAAGTTAC	1020
AAAGGCTGAA AAAGTTGCAG CTAATACAGA TGCTAAACAA AGTGAAGTTA ACGAAGCTGT	1080
TGAAAAATTA ACTGCAACTA TTGAAAAATT GGTTGAATTA TCTGAAAAGC CAATATTAAC	1140
ATTGACTAGT ACCGATAAGA AAATATTGGA ACGTGAAGCT GTTGCTAAGT ATACTCTAGA	1200
AAATCAAAAC AAAACAAAAA TCAAATCAAT CACAGCTGAA TTGAAAAAAG GAGAAGAAGT	1260
TATTAATACT GTAGTCCTTA CAGATGACAA GGTAACAACA GAACTATAA GCGCTGCATT	1320
TAAGAACCTA GAGTACTACA AAGAATACAC CCTATCTACA ACTATGATTT ACGACAGAGG	1380
TAACGGTGAA GAACTGAAA CTCTAGAAAA TCAAAATATT CAATTAGATC TTAAAAAAGT	1440
TGAGCTTAAA AATATTAAAC GTACAGATTT AATCAAATAC GAAAATGGAA AAGAACTAA	1500
TGAATCACTG ATAACAATA TTCCTGATGA TAAGAGCAAT TATTATTTAA AAATAACTTC	1560
AAATAATCAG AAAACTACAT TACTAGCTGT TAAAAATATA GAAGAACTA CGGTTAACGG	1620
AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA	1680
TAAATTTGAA GAAGAA	1696

## (2) INFORMATION FOR SEQ ID NO:218:


## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 565 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:



Val	Val	Glu	Val	Glu	Thr	Pro	Gln	Ser	Ile	Thr	Asn	Gln	Glu	Gln	Ala	1	5	10	15
Arg	Thr	Glu	Asn	Gln	Val	Val	Glu	Thr	Glu	Glu	Ala	Pro	Lys	Glu	Glu	20	25	30	
Ala	Pro	Lys	Thr	Glu	Glu	Ser	Pro	Lys	Glu	Glu	Pro	Lys	Ser	Glu	Val	35	40	45	
Lys	Pro	Thr	Asp	Asp	Thr	Leu	Pro	Lys	Val	Glu	Glu	Gly	Lys	Glu	Asp	50	55	60	
Ser	Ala	Glu	Pro	Ala	Pro	Val	Glu	Glu	Val	Gly	Gly	Glu	Val	Glu	Ser	65	70	75	80
Lys	Pro	Glu	Glu	Lys	Val	Ala	Val	Lys	Pro	Glu	Ser	Gln	Pro	Ser	Asp	85	90	95	
Lys	Pro	Ala	Glu	Glu	Ser	Lys	Val	Glu	Gln	Ala	Gly	Glu	Pro	Val	Ala	100	105	110	
Pro	Arg	Glu	Asp	Glu	Lys	Ala	Pro	Val	Glu	Pro	Glu	Lys	Gln	Pro	Glu	115	120	125	
Ala	Pro	Glu	Glu	Glu	Lys	Ala	Val	Glu	Glu	Thr	Pro	Lys	Gln	Glu	Glu	130	135	140	
Ser	Thr	Pro	Asp	Thr	Lys	Ala	Glu	Glu	Thr	Val	Glu	Pro	Lys	Glu	Glu	145	150	155	160
Thr	Val	Asn	Gln	Ser	Ile	Glu	Gln	Pro	Lys	Val	Glu	Thr	Pro	Ala	Val	165	170	175	
Glu	Lys	Gln	Thr	Glu	Pro	Thr	Glu	Glu	Pro	Lys	Val	Glu	Gln	Ala	Gly	180	185	190	
Glu	Pro	Val	Ala	Pro	Arg	Glu	Asp	Glu	Gln	Ala	Pro	Thr	Ala	Pro	Val	195	200	205	
Glu	Pro	Glu	Lys	Gln	Pro	Glu	Val	Pro	Glu	Glu	Glu	Lys	Ala	Val	Glu	210	215	220	
Glu	Thr	Pro	Lys	Pro	Glu	Asp	Lys	Ile	Lys	Gly	Ile	Gly	Thr	Lys	Glu	225	230	235	240
Pro	Val	Asp	Lys	Ser	Glu	Leu	Asn	Asn	Gln	Ile	Asp	Lys	Ala	Ser	Ser	245	250	255	
Val	Ser	Pro	Thr	Asp	Tyr	Ser	Thr	Ala	Ser	Tyr	Asn	Ala	Leu	Gly	Pro	260	265	270	
Val	Leu	Glu	Thr	Ala	Lys	Gly	Val	Tyr	Ala	Ser	Glu	Pro	Val	Lys	Gln	275	280	285	
Pro	Glu	Val	Asn	Ser	Glu	Thr	Asn	Lys	Leu	Lys	Thr	Ala	Ile	Asp	Ala				

290	295	300
Leu 305	Asn Val Asp Lys Thr 310	Glu Leu Asn Asn Thr 315
Thr 320	Lys Val Lys Glu 325	His Tyr Ser Asp Arg 330
Thr 335	Glu Val Thr 340	Lys Ala Glu Lys Val 345
Gln 350	Ser Glu Val Asn Glu 355	Ala Val Glu Lys Leu Thr 360
Lys 365	Leu Val Glu Leu Ser 370	Glu Lys Pro Ile Leu Thr 380
Asp 385	Lys Lys Ile Leu Glu 390	Arg Glu Ala Val Ala 395
Asn 400	Gln Asn Lys Thr 405	Lys Ile Lys Ser Ile 410
Gly 415	Glu Glu Val Ile Asn Thr 420	Val Val Leu Thr Asp 425
Thr 430	Glu Thr Ile Ser Ala 435	Ala Phe Lys Asn Leu Glu 440
Tyr 445	Thr Leu Ser Thr Thr 450	Met Ile Tyr Asp Arg 455
Glu 460	Thr Glu Thr Leu Glu 465	Asn Gln Asn Ile Gln 470
Glu 475	Glu Thr Lys Asn Ile Lys 480	Arg Thr Asp Leu Ile 485
Asn 490	Lys Glu Thr Asn Glu 495	Ser Leu Ile Thr Thr 500
Lys 505	Asn Tyr Tyr Leu Lys 510	Ile Thr Ser Asn Asn 515
Thr 520	Ala Val Lys Asn Ile Glu 525	Glu Glu Thr Thr Val 530
Thr 535	Lys Val Thr Ala Ile 540	Ala Asp Asn Leu Val 545
Asn 550	Lys Phe Glu Glu Glu 555	

## (2) INFORMATION FOR SEQ ID NO: 219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:



AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA 60  
 TAAATTTGAA GAAGAATACG TTCACTATAT TGAAAAACCT AAAGTCCACG AAGATAATGT 120  
 ATATTATAAT TTCAAAGAAT TAGTGGAAGC TATTCAAAAC GATCCTTCAA AAGAATATCG 180  
 TCTGGGACAA TCAATGAGCG CTAGAAATGT TGTTCCTAAT GGAAAATCAT ATATCACTAA 240  
 AGAATTCACA GGAAAACTTT TAAGTTCTGA AGGAAAACAA TTTGCTATTA CTGAATTGGA 300  
 ACATCCATTA TTTAATGTGA TAACAAACGC AACGATAAAT AATGTGAATT TTGAAAATGT 360  
 AGAGATAGAA CGTTCTGGTC AAGATAATAT TGCATCATTG GCCAATACTA TGAAAGGTTT 420  
 TTCAGTTATT ACAAATGTCA AAATTACAGG CACACTTTCA GGTGCTAATA ATGTTGCTGG 480  
 ATTTGTAAAT AATATGAATG ATGGAACCTG TATTGAAAAT GTTGCTTTCT TTGGCAAAC 540  
 ACACTCTACA AGTGGAAATG GCTCTCATA AGGGGGAATT GCAGGTACAA ACTATAGAGG 600  
 AATTGTTAGA AAAGCATATG TTGATGCTAC TATTACAGGA AACAAAACAC GCGCCAGCTT 660  
 GTTAGTTCCT AAAGTAGATT ATGGATTAAC TCTAGACCAT CTTATTGGTA CAAAAGCTCT 720  
 CCTAACTGAG TCGGTTGTAA AAGGTAAAAT AGATGTTTCA AATCCAGTAG AAGTTGGAGC 780  
 AATAGCAAGT AAGACTTGGC CTGTAGGTAC GGTAAGTAAT TCTGTCAGCT ATGCTAAGAT 840  
 TATCCGTGGA GAGGAGTTAT TCGGCTCTAA CGACGTTGAT GATTCTGATT ATGCTAGTGC 900  
 TCATATAAAA GATTTATATG CGGTAGAGGG ATATTCGTCA GGTAATAGAT CATTTAGGAA 960  
 ATCTAAAACA TTTACTAAAT TAACTAAAGA ACAAGCTGAT GCTAAAGTTA CTACTTTCAA 1020  
 TATTACTGCT GATAAATTAG AAAGTGATCT ATCTCCTCTT GCAAACTTA ATGAAGAAAA 1080  
 AGCCTATTCT AGTATTCAAG ATTATAACGC TGAATATAAC CAAGCCTATA AAAATCTTGA 1140  
 AAAATTAATA CCATTCTACA ATAAAGATTA TATTGTATAT CAAGGTAATA AATTAAATAA 1200  
 AGAACACCAT CTAAATACTA AAGAAGTTCT TTCTGTTACC GCGATGAACA ACAATGAGTT 1260  
 TATCACAAAC CTAGATGAAG CTAATAAAAT TATTGTTTAC TATGCGGACG GTACAAAAGA 1320  
 TTACTTTAAC TTGCTTTCTA GCAGTGAAGG TTTAAGTAAT GTAAAAGAAT ATACTATAAC 1380  
 TGACTTAGGA ATTAAATATA CACCTAATAT CGTTCAAAAA GATAACACTA CTCTTGTTAA 1440  
 TGATATAAAA TCTATTTTAG AATCAGTAGA GCTTCAGTCT CAAACGATGT ATCAGCATCT 1500  
 AAATCGATTA GGTGACTATA GAGTTAATGC AATCAAAGAT TTATATTTAG AAGAAAGCTT 1560  
 CACAGATGTT AAAGAAAAC TAAACAAACCT AATCACAAAA TTAGTTCAAA ACGAAGAACA 1620  
 TCAACTAAAT GATTCTCCAG CTGCTCGTCA AATGATTCGT GATAAAGTCG AGAAAAACAA 1680  
 AGCAGCTTTA TTACTAGGTT TAACTTACCT AAATCGTTAC TATGGAGTTA AATTTGGTGA 1740  
 TGTTAATATT AAAGAATTAA TGCTATTCAA ACCAGATTTT TATGGTGAAA AAGTTAGCGT 1800  
 ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT 1860  
 CGACGCATTC GGTCAAGTA 1879

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Thr Pro Val Tyr Lys Val Thr Ala Ile Ala Asp Asn Leu Val Ser Arg  
 1 5 10 15  
 Thr Ala Asp Asn Lys Phe Glu Glu Glu Tyr Val His Tyr Ile Glu Lys  
 20 25 30  
 Pro Lys Val His Glu Asp Asn Val Tyr Tyr Asn Phe Lys Glu Leu Val  
 35 40 45  
 Glu Ala Ile Gln Asn Asp Pro Ser Lys Glu Tyr Arg Leu Gly Gln Ser  
 50 55 60  
 Met Ser Ala Arg Asn Val Val Pro Asn Gly Lys Ser Tyr Ile Thr Lys  
 65 70 75 80  
 Glu Phe Thr Gly Lys Leu Leu Ser Ser Glu Gly Lys Gln Phe Ala Ile  
 85 90 95  
 Thr Glu Leu Glu His Pro Leu Phe Asn Val Ile Thr Asn Ala Thr Ile  
 100 105 110  
 Asn Asn Val Asn Phe Glu Asn Val Glu Ile Glu Arg Ser Gly Gln Asp  
 115 120 125  
 Asn Ile Ala Ser Leu Ala Asn Thr Met Lys Gly Ser Ser Val Ile Thr  
 130 135 140  
 Asn Val Lys Ile Thr Gly Thr Leu Ser Gly Arg Asn Asn Val Ala Gly  
 145 150 155 160  
 Phe Val Asn Asn Met Asn Asp Gly Thr Arg Ile Glu Asn Val Ala Phe  
 165 170 175  
 Phe Gly Lys Leu His Ser Thr Ser Gly Asn Gly Ser His Thr Gly Gly  
 180 185 190  
 Ile Ala Gly Thr Asn Tyr Arg Gly Ile Val Arg Lys Ala Tyr Val Asp  
 195 200 205  
 Ala Thr Ile Thr Gly Asn Lys Thr Arg Ala Ser Leu Leu Val Pro Lys  
 210 215 220  
 Val Asp Tyr Gly Leu Thr Leu Asp His Leu Ile Gly Thr Lys Ala Leu  
 225 230 235 240  
 Leu Thr Glu Ser Val Val Lys Gly Lys Ile Asp Val Ser Asn Pro Val  
 245 250 255  
 Glu Val Gly Ala Ile Ala Ser Lys Thr Trp Pro Val Gly Thr Val Ser  
 260 265 270

Asn Ser Val Ser Tyr Ala Lys Ile Ile Arg Gly Glu Glu Leu Phe Gly  
 275 280 285  
 Ser Asn Asp Val Asp Asp Ser Asp Tyr Ala Ser Ala His Ile Lys Asp  
 290 295 300  
 Leu Tyr Ala Val Glu Gly Tyr Ser Ser Gly Asn Arg Ser Phe Arg Lys  
 305 310 315 320  
 Ser Lys Thr Phe Thr Lys Leu Thr Lys Glu Gln Ala Asp Ala Lys Val  
 325 330 335  
 Thr Thr Phe Asn Ile Thr Ala Asp Lys Leu Glu Ser Asp Leu Ser Pro  
 340 345 350  
 Leu Ala Lys Leu Asn Glu Glu Lys Ala Tyr Ser Ser Ile Gln Asp Tyr  
 355 360 365  
 Asn Ala Glu Tyr Asn Gln Ala Tyr Lys Asn Leu Glu Lys Leu Ile Pro  
 370 375 380  
 Phe Tyr Asn Lys Asp Tyr Ile Val Tyr Gln Gly Asn Lys Leu Asn Lys  
 385 390 395 400  
 Glu His His Leu Asn Thr Lys Glu Val Leu Ser Val Thr Ala Met Asn  
 405 410 415  
 Asn Asn Glu Phe Ile Thr Asn Leu Asp Glu Ala Asn Lys Ile Ile Val  
 420 425 430  
 His Tyr Ala Asp Gly Thr Lys Asp Tyr Phe Asn Leu Ser Ser Ser Ser  
 435 440 445  
 Glu Gly Leu Ser Asn Val Lys Glu Tyr Thr Ile Thr Asp Leu Gly Ile  
 450 455 460  
 Lys Tyr Thr Pro Asn Ile Val Gln Lys Asp Asn Thr Thr Leu Val Asn  
 465 470 475 480  
 Asp Ile Lys Ser Ile Leu Glu Ser Val Glu Leu Gln Ser Gln Thr Met  
 485 490 495  
 Tyr Gln His Leu Asn Arg Leu Gly Asp Tyr Arg Val Asn Ala Ile Lys  
 500 505 510  
 Asp Leu Tyr Leu Glu Glu Ser Phe Thr Asp Val Lys Glu Asn Leu Thr  
 515 520 525  
 Asn Leu Ile Thr Lys Leu Val Gln Asn Glu Glu His Gln Leu Asn Asp  
 530 535 540  
 Ser Pro Ala Ala Arg Gln Met Ile Arg Asp Lys Val Glu Lys Asn Lys  
 545 550 555 560  
 Ala Ala Leu Leu Leu Gly Leu Thr Tyr Leu Asn Arg Tyr Tyr Gly Val  
 565 570 575  
 Lys Phe Gly Asp Val Asn Ile Lys Glu Leu Met Leu Phe Lys Pro Asp  
 580 585 590  
 Phe Tyr Gly Glu Lys Val Ser Val Leu Asp Arg Leu Ile Glu Ile Gly  
 595 600 605

Ser Lys Glu Asn Asn Ile Lys Gly Ser Arg Thr Phe Asp Ala Phe Gly  
 610 615 620

Gln Val  
 625

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT 60  
 CGACGCATTC GGTCAAGTAT TGGCTAAATA TACTAAATCA GGTAATTTAG ATGCATTTTTT 120  
 AAATTATAAT AGACAAATTGT TCACAAATAT AGACAATATG AACGATTGGT TTATTGATGC 180  
 TACAGAAGAC CATGTCTACA TCGCAGAACG CGCTTCTGAG GTCGAAGAAA TTAAAAATTC 240  
 TAAACATCGT GCATTTCGATA ATTTAAAACG AAGTCACCTT AGAAATACTA TACTCCCACT 300  
 ACTGAATATT GATAAAGCAC ATCTTTATTT AATTTCAAAT TATAATGCAA TTGCCTTTGG 360  
 TAGTGCAGAG CGATTAGGTA AAAAATCATT AGAAGATATT AAAGATATCG TTAACAAAGC 420  
 TGCAGATGGT TATAGAAACT ATTATGATTT CTGGTATCGT CTAGCGTCTG ATAACGTTAA 480  
 ACAACGACTA CTAAGAGATG CTGTTATTCC TATTTGGGAA GGTTATAACG CTCCTGGTGG 540  
 ATGGGTTGAA AAATATGGCC GCTATAATAC CGACAAAGTA TATACTCCTC TTAGAGAATT 600  
 CTTTGGTCCT ATGGATAAGT ATTATAATTA TAATGGAACA GGAGCTTATG CTGCTATATA 660  
 TCCTAACTCT GATGATATTA GAACTGATGT AAAATATGTT CATTTAGAAA TGGTTGGTGA 720  
 ATACGGTATT TCAGTTTACA CACATGAAAC AACACACGTC AACGACCGTG CGATTTACTT 780  
 AGGTGGCTTT GGACACCGTG AAGGTACTGA TGCTGAAGCA TATGCTCAGG GTATGCTACA 840  
 AACTCCTGTT ACTGGTAGTG GATTTGATGA GTTTGGTTCT TTAGGTATTA ATATGGTATT 900  
 TAAACGCAA AATGATGGGA ATCAGTGGTA TATTACAGAT CCAAAAACCTC TAAAAACACG 960  
 AGAAGATATT AATAGATATA TGAAGGGTTA TAATGACACT TTAACCTTC TTGATGAAAT 1020  
 TGAGGCTGAA TCTGTGATTT CTCAACAAAA TAAAGATTTA AATAGTGCAT GGTTCAAAAA 1080  
 AATAGATAGA GAATACCGTG ATAACAATAA ATTAAATCAA TGGGATAAAA TTCGAAATCT 1140  
 AAGTCAAGAA GAGAAAAATG AATTAAATAT TCAATCTGTT AATGATTTAG TTGATCAACA 1200  
 ATTAATGACT AATCGCAATC CAGGTAATGG TATCTATAAA CCCGAAGCAA TTAGCTATAA 1260  
 CGATCAATCA CCTTATGTAG GTGTTAGAAT GATGACCGGT ATCTACGGAG GTAATACTAG 1320  
 TAAAGGTGCT CCTGGAGCTG TTTCATTCAA ACATAATGCT TTTAGATTAT GGGGTTACTA 1380

CGGATACGAA AATGGGTTCT TAGGTTATGC TTCAAATAAA TATAACAAC AATCTAAAC	1440
AGATGGTGAG TCTGTTCTAA GTGATGAATA TATTATCAAG AAAATATCTA ACAATACATT	1500
TAATACTATT GAAGAATTTA AAAAAGCTTA CTTCAAAGAA GTTAAAGATA AAGCAACGAA	1560
AGGATTAACA ACATTCGAAG TAAATGGTTC TTCCGTTTCA TCATACGATG ATTTACTGAC	1620
ATTGTTTAAA GAAGCTGTTA AAAAAGATGC CGAAACTCTT AAACAAGAAG CAAACGGTAA	1680
TAAAACAGTA TCTATGAATA ATACAGTTAA ATTAAAAGAA GCTGTTTATA AGAAACTTCT	1740
TCAACAAACA AATAGCTTTA AACTTCAAT CTTTAAA	1777


## (2) INFORMATION FOR SEQ ID NO:222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:



Leu	Asp	Arg	Leu	Ile	Glu	Ile	Gly	Ser	Lys	Glu	Asn	Asn	Ile	Lys	Gly	1	5	10	15
Ser	Arg	Thr	Phe	Asp	Ala	Phe	Gly	Gln	Val	Leu	Ala	Lys	Tyr	Thr	Lys	20	25	30	
Ser	Gly	Asn	Leu	Asp	Ala	Phe	Leu	Asn	Tyr	Asn	Arg	Gln	Leu	Phe	Thr	35	40	45	
Asn	Ile	Asp	Asn	Met	Asn	Asp	Trp	Phe	Ile	Asp	Ala	Thr	Glu	Asp	His	50	55	60	
Val	Tyr	Ile	Ala	Glu	Arg	Ala	Ser	Glu	Val	Glu	Glu	Ile	Lys	Asn	Ser	65	70	75	80
Lys	His	Arg	Ala	Phe	Asp	Asn	Leu	Lys	Arg	Ser	His	Leu	Arg	Asn	Thr	85	90	95	
Ile	Leu	Pro	Leu	Leu	Asn	Ile	Asp	Lys	Ala	His	Leu	Tyr	Leu	Ile	Ser	100	105	110	
Asn	Tyr	Asn	Ala	Ile	Ala	Phe	Gly	Ser	Ala	Glu	Arg	Leu	Gly	Lys	Lys	115	120	125	
Ser	Leu	Glu	Asp	Ile	Lys	Asp	Ile	Val	Asn	Lys	Ala	Ala	Asp	Gly	Tyr	130	135	140	
Arg	Asn	Tyr	Tyr	Asp	Phe	Trp	Tyr	Arg	Leu	Ala	Ser	Asp	Asn	Val	Lys	145	150	155	160
Gln	Arg	Leu	Leu	Arg	Asp	Ala	Val	Ile	Pro	Ile	Trp	Glu	Gly	Tyr	Asn	165	170	175	
Ala	Pro	Gly	Gly	Trp	Val	Glu	Lys	Tyr	Gly	Arg	Tyr	Asn	Thr	Asp	Lys	180	185	190	
Val	Tyr	Thr	Pro	Leu	Arg	Glu	Phe	Phe	Gly	Pro	Met	Asp	Lys	Tyr	Tyr				

195                      200                      205  
 Asn Tyr Asn Gly Thr Gly Ala Tyr Ala Ala Ile Tyr Pro Asn Ser Asp  
     210                      215                      220  
 Asp Ile Arg Thr Asp Val Lys Tyr Val His Leu Glu Met Val Gly Glu  
     225                      230                      235                      240  
 Tyr Gly Ile Ser Val Tyr Thr His Glu Thr Thr His Val Asn Asp Arg  
                     245                      250                      255  
 Ala Ile Tyr Leu Gly Gly Phe Gly His Arg Glu Gly Thr Asp Ala Glu  
                     260                      265                      270  
 Ala Tyr Ala Gln Gly Met Leu Gln Thr Pro Val Thr Gly Ser Gly Phe  
                     275                      280                      285  
 Asp Glu Phe Gly Ser Leu Gly Ile Asn Met Val Phe Lys Arg Lys Asn  
     290                      295                      300  
 Asp Gly Asn Gln Trp Tyr Ile Thr Asp Pro Lys Thr Leu Lys Thr Arg  
     305                      310                      315                      320  
 Glu Asp Ile Asn Arg Tyr Met Lys Gly Tyr Asn Asp Thr Leu Thr Leu  
                     325                      330                      335  
 Leu Asp Glu Ile Glu Ala Glu Ser Val Ile Ser Gln Gln Asn Lys Asp  
                     340                      345                      350  
 Leu Asn Ser Ala Trp Phe Lys Lys Ile Asp Arg Glu Tyr Arg Asp Asn  
                     355                      360                      365  
 Asn Lys Leu Asn Gln Trp Asp Lys Ile Arg Asn Leu Ser Gln Glu Glu  
     370                      375                      380  
 Lys Asn Glu Leu Asn Ile Gln Ser Val Asn Asp Leu Val Asp Gln Gln  
     385                      390                      395                      400  
 Leu Met Thr Asn Arg Asn Pro Gly Asn Gly Ile Tyr Lys Pro Glu Ala  
                     405                      410                      415  
 Ile Ser Tyr Asn Asp Gln Ser Pro Tyr Val Gly Val Arg Met Met Thr  
                     420                      425                      430  
 Gly Ile Tyr Gly Gly Asn Thr Ser Lys Gly Ala Pro Gly Ala Val Ser  
                     435                      440                      445  
 Phe Lys His Asn Ala Phe Arg Leu Trp Gly Tyr Tyr Gly Tyr Glu Asn  
     450                      455                      460  
 Gly Phe Leu Gly Tyr Ala Ser Asn Lys Tyr Lys Gln Gln Ser Lys Thr  
     465                      470                      475                      480  
 Asp Gly Glu Ser Val Leu Ser Asp Glu Tyr Ile Ile Lys Lys Ile Ser  
                     485                      490                      495  
 Asn Asn Thr Phe Asn Thr Ile Glu Glu Phe Lys Lys Ala Tyr Phe Lys  
                     500                      505                      510  
 Glu Val Lys Asp Lys Ala Thr Lys Gly Leu Thr Thr Phe Glu Val Asn  
                     515                      520                      525  
 Gly Ser Ser Val Ser Ser Tyr Asp Asp Leu Leu Thr Leu Phe Lys Glu  
     530                      535                      540

Ala Val Lys Lys Asp Ala Glu Thr Leu Lys Gln Glu Ala Asn Gly Asn  
545 550 555 560

Lys Thr Val Ser Met Asn Asn Thr Val Lys Leu Lys Glu Ala Val Tyr  
565 570 575

Lys Lys Leu Leu Gln Gln Thr Asn Ser Phe Lys Thr Ser Ile Phe Lys  
580 585 590

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

TAAGACAGAT GAACGGAGCA AGGTGTTTGA CTTTTCATT CCCTACTATA CTGCAAAAAA 60  
TAAACTCATT GTCAAAAAAT CTGACTTGAC TACTTATCAG TCTGTAAACG ACTTGCGCGCA 120  
GAAAAAGGTT GGAGCGCAGA AAGGTTCGAT TCAAGAGACG ATGGCGAAAG ATTTGCTACA 180  
AAATTCTTCC CTCGTATCTC TGCCTAAAAA TGGGAATTTA ATCACAGATT TAAAATCAGG 240  
ACAAGTGGAT GCCGTTATCT TTGAAGAACC TGTTTCCAAG GGATTGTGG AAAATAATCC 300  
TGATTTAGCA ATCGCAGACC TCAATTTTGA AAAAGAGCAA GATGATTCCT ACGCGGTAGC 360  
CATgAAAAAA GATAGCAAGA AATTGAAGAG GCAGTTCGAT AAAACCATTC AAAAGTTGAA 420  
GGAGTCTGGG GAATTAGACA AACTCATTGA GGAAGCCTTA 460

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Lys Thr Asp Glu Arg Ser Lys Val Phe Asp Phe Ser Ile Pro Tyr Tyr  
1 5 10 15

Thr Ala Lys Asn Lys Leu Ile Val Lys Lys Ser Asp Leu Thr Thr Tyr  
20 25 30

Gln Ser Val Asn Asp Leu Ala Gln Lys Lys Val Gly Ala Gln Lys Gly  
35 40 45

Ser Ile Gln Glu Thr Met Ala Lys Asp Leu Leu Gln Asn Ser Ser Leu  
50 55 60

Val Ser Leu Pro Lys Asn Gly Asn Leu Ile Thr Asp Leu Lys Ser Gly

65		70		75		80
Gln Val Asp Ala Val Ile Phe Glu Glu Pro Val Ser Lys Gly Phe Val						
		85		90		95
Glu Asn Asn Pro Asp Leu Ala Ile Ala Asp Leu Asn Phe Glu Lys Glu						
		100		105		110
Gln Asp Asp Ser Tyr Ala Val Ala Met Lys Lys Asp Ser Lys Lys Leu						
		115		120		125
Lys Arg Gln Phe Asp Lys Thr Ile Gln Lys Leu Lys Glu Ser Gly Glu						
		130		135		140
Leu Asp Lys Leu Ile Glu Glu Ala Leu						
		145		150		

## (2) INFORMATION FOR SEQ ID NO: 225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

CTGTGAGAAT CAAGCTACAC CCAAAGAGAC TAGCGCTCAA AAGACAATCG TCCTTGCTAC	60
AGCTGGCGAC GTGCCACCAT TTGACTACGA AGACAAGGGC AATCTGACAG GCTTTGATAT	120
CGAAGTTTTA AAGGCAGTAG ATGAAAAACT CAGCGACTAC GAGATTCAAT TCCAAAGAAC	180
CGCCTGGGAG AGCATCTTCC CAGGACTTGA TTCTGGTCAC TATCAGGCTG CGGCCAATAA	240
CTTGAGTTAC ACAAAGAGC GTGCTGAAAA ATACCTTTAC TCGCTTCCAA TTTCCAACAA	300
TCCCCTCGTC CTTGTCAGCA ACAAGAAAAA TCCTTTGACT TCTCTTGACC AGATCGCTGG	360
TAAACAACA CAAGAGGATA CCGGAAC TTC TAACGCTCAA TTCATCAATA ACTGGAATCA	420
GAAACACACT GATAATCCCG CTACAATTAA TTTTCTGGT GAGGATATTG GTAAACGAAT	480
CCTAGACCTT GCTAACGGAG AGTTTGATTT CCTAGTTTTT GACAAGGTAT CCGTTCAAAA	540
GATTATCAAG GACCGTGGTT TAGACCTCTC AGTCGTTGAT TTACCTTCTG CAGATAGCCC	600
CAGCAATTAT ATCATTTTCT CAAGCGACCA AAAAGAGTTT AAAGAGCAAT TTGATAAAGC	660
GCTCAAAGAA CTCTATCAAG ACGGAACCC TGA AAAACTC AGCAATACCT ATCTAGGTGG	720
TTCTTACCTC CCAGATCAAT CTCAGTTACA A	751

## (2) INFORMATION FOR SEQ ID NO: 226:


## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:



Cys	Glu	Asn	Gln	Ala	Thr	Pro	Lys	Glu	Thr	Ser	Ala	Gln	Lys	Thr	Ile	1	5	10	15
Val	Leu	Ala	Thr	Ala	Gly	Asp	Val	Pro	Pro	Phe	Asp	Tyr	Glu	Asp	Lys	20	25	30	
Gly	Asn	Leu	Thr	Gly	Phe	Asp	Ile	Glu	Val	Leu	Lys	Ala	Val	Asp	Glu	35	40	45	
Lys	Leu	Ser	Asp	Tyr	Glu	Ile	Gln	Phe	Gln	Arg	Thr	Ala	Trp	Glu	Ser	50	55	60	
Ile	Phe	Pro	Gly	Leu	Asp	Ser	Gly	His	Tyr	Gln	Ala	Ala	Ala	Asn	Asn	65	70	75	80
Leu	Ser	Tyr	Thr	Lys	Glu	Arg	Ala	Glu	Lys	Tyr	Leu	Tyr	Ser	Leu	Pro	85	90	95	
Ile	Ser	Asn	Asn	Pro	Leu	Val	Leu	Val	Ser	Asn	Lys	Lys	Asn	Pro	Leu	100	105	110	
Thr	Ser	Leu	Asp	Gln	Ile	Ala	Gly	Lys	Thr	Thr	Gln	Glu	Asp	Thr	Gly	115	120	125	
Thr	Ser	Asn	Ala	Gln	Phe	Ile	Asn	Asn	Trp	Asn	Gln	Lys	His	Thr	Asp	130	135	140	
Asn	Pro	Ala	Thr	Ile	Asn	Phe	Ser	Gly	Glu	Asp	Ile	Gly	Lys	Arg	Ile	145	150	155	160
Leu	Asp	Leu	Ala	Asn	Gly	Glu	Phe	Asp	Phe	Leu	Val	Phe	Asp	Lys	Val	165	170	175	
Ser	Val	Gln	Lys	Ile	Ile	Lys	Asp	Arg	Gly	Leu	Asp	Leu	Ser	Val	Val	180	185	190	
Asp	Leu	Pro	Ser	Ala	Asp	Ser	Pro	Ser	Asn	Tyr	Ile	Ile	Phe	Ser	Ser	195	200	205	
Asp	Gln	Lys	Glu	Phe	Lys	Glu	Gln	Phe	Asp	Lys	Ala	Leu	Lys	Glu	Leu	210	215	220	
Tyr	Gln	Asp	Gly	Thr	Leu	Glu	Lys	Leu	Ser	Asn	Thr	Tyr	Leu	Gly	Gly	225	230	235	240
Ser	Tyr	Leu	Pro	Asp	Gln	Ser	Gln	Leu	Gln							245	250		

## (2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

GACTGGATCC TAAAATCTAC GACAATAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

CTGAGTCGAC TGGTTGTGCT GGTGAG

27

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

GTCAGGATCC AAATTACAAT ACGGACTATG

30

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CAGTGTCGAC TAACTCTAGG TCGGAAAC

28

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GACTGGATCC TGAGAATCAA GCTACACCCA AAGAG

35

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AGTCAAGCTT TTGTAAGTGA GATTGATCTG G

31

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GACTGGATCC TGGTAACCGC TCTTCTCGTA ACGCAGC

37

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

AGTCAAGCTT TTTCAGGAAC TTTTACGCTT CC

32

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

AGTCAGATCT TGTGGAAATT TGACAGGTAA CAGCAAAAAA GCTGC

45

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

ACTGAAGCTT TTTTGT TTTT CAAGAATTCA TCG

33

## (2) INFORMATION FOR SEQ ID NO: 237:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

GACTGGATCC TGGTCAAGGA ACTGCTTCTA AAGAC

35

## (2) INFORMATION FOR SEQ ID NO: 238:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

AGTCAAGCTT TCACAAATTC GTTGGTGAAG CC

32

## (2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

GACTGGATCC TAGCTCAGGT GGAAACGCTG GTTCATCC

38

## (2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

AGTCAAGCTT ATCAACTTTT CCACCTTCAA CAACC

35

## (2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

GTCAAGATCT CTCCAACATAT GGTAAATCTG CGGATGG

37

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

AGTCCTGCAG ATCCACATCC GCTTTCATCG GGTAAAGAA GG

42

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

GACTGGATCC TGGGAAAAAT TCTAGCGAAA CTAGTGG

37

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

GTCACCTGCAG CTGTCCTTCT TTTACTTCTT TGGTTGC

37

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

GACTGGATCC TGCTAGCGGA AAAAAAGATA CAACTTCTGG

40

(2) INFORMATION FOR SEQ ID NO: 246:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

CTGAAAGCTT TTTTGCCAAT CCTTCAGCAA TCTTGTC

37

(2) INFORMATION FOR SEQ ID NO: 247:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

GACTAGATCT TGGCTCAAAA AATACAGCTT CAAGTCC

37

(2) INFORMATION FOR SEQ ID NO: 248:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

AGTCCTGCAG GTTTTTGTTT GCTTGGTATT GGTCG

35

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

GACTGGATCC TAGTACAAAC TCAAGCACTA GTCAGACAGA G

41

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CAGTCTGCAG TTTCAAAGCT TTTTGTATGT CTTC

34

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

GACTGGATCC TGGCAATTCT GGCGGAAGTA AAGATGC

37

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

AGTCAAGCTT GTTTCATAGC TTTTTTGATT GTTTCG

36

(2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

GACTGGATCC TTCACAAGAA AAAACAAAAA ATGAAGATGG

40

(2) INFORMATION FOR SEQ ID NO: 254:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

AGTCAAGCTT ATCGACGTAG TCTCCGCCTT C

31

(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

GACTGGATCC GAAAGGTCTG TGGTCAAATA ATCTTACC

38

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

AGTCAAGCTT AGAGTTAACA TGGTGCTTGC CAATAGG

37

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GACTGGATCC AAACCTCAGAA AAGAAAGCAG ACAATGC

37

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AGTCAAGCTT CCAAACCTGGT TGATCCAAAC CATCTG

36

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:



GACTGGATCC TTCGAAAGGG TCAGAAGGTG CAGACC

36

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AGTCAAGCTT CTGTAGGCTT GGTGTGCCCC AGTTGC

36

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTGAGGATCC GGGGATGGCA GCTTTTAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 262:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CAGTAAGCTT GTTTACCCAT TCACCATTAC C

31

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CAGTGGATCC AGACGAGCAA AAAATTAAG

29

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

TCAGAAGCTT GTTTACCCAT TCACCATT

28

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

GACTGGATCC CTGTGGTGAG GAAGAACTA AAAAG

35

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

CTGAGTCGAC AATATTCTGT AGGAATGCTT CGAATTG

38

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

CTGAGGATCC GACTTTTAAC AATAAACTA TTGAAGAG

38

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

GTCAGTGCAG GTTGTCACCT CCAAAAATCA CGG

33

## (2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GACTGGATCC CTTTACAGGT AAACAAC TAC AAGTCGG

37

## (2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

CAGTAAGCTT TTCGAAGTTT GGCTCAGAAT TG

32

## (2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

GACTGGATCC CCAGGCTGAT ACAAGTATCG CA

32

## (2) INFORMATION FOR SEQ ID NO: 272:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CAGTAAGCTT ATCTGCAGTA TGGCTAGATG G

31

## (2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

GACTGGATCC GTCTGTATCA TTTGAAAACA AAGAAAC

37

(2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CAGTCTGCAG TTTTACTGTT GCTGTGCTTG TG

32

(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ACTGAGATCT TGGTCAAAAG GAAAGTCAGA CAGGAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 41 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CAGTAAGCTT ATTCCTGAGC TTTTTTGATA AAGGTTGCGC A

41

(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

ACTGGGATCC GAAGGATAGA TATATTTTAG CATTTGAGAC

40

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

AGTCAAGCTT CCATGGTATC AAAGGCAAGA CTGG

35

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

GTCAGGATCC GGTA GTTAA GTTGGTATTA ACGG

34

(2) INFORMATION FOR SEQ ID NO: 280:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

AGTCAAGCTT GCAATTTTTG CGAAGTATTC CAAGAG

36

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear


(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

AGTCGGATCC TTCTTACGAG TTGGGACTGT ATCAAGC

37

(2) INFORMATION FOR SEQ ID NO: 282:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:  
AGTCAAGCTT GTTTATTTTT TCCTTACTTA CAGATGAAGG 40
- (2) INFORMATION FOR SEQ ID NO: 283:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:  
AGTCGGATCC TACTGAGATG CATCATAATC TAGGAGC 37
- (2) INFORMATION FOR SEQ ID NO: 284:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
-  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:  
TCAGCTCGAG TTCTTTGACA TCTCCATCAT AAGTCGC 37
- (2) INFORMATION FOR SEQ ID NO: 285:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:  
GACTGGATCC GGTTTTGAGA AAGTATTTGC AGGGG 35
- (2) INFORMATION FOR SEQ ID NO: 286:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:  
CAGTAAGCTT GGATTTTTTC ATGGATGCAA TTTTTTTTGG 39
- (2) INFORMATION FOR SEQ ID NO: 287:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GACTGGATCC GACAACATTT ACTATCCATA CAGTAGAGTC AGC

43

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

GACTAAGCTT GGCATAAGGT TGCAATTCTG GATTAATTGG

40

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

GACTGGATCC GGCTAAGGAA AGAGTGGATG

30

(2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GACTAAGCTT TTCATTTTTA AATTGACTAT GCGCCCCG

37

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

GACTGGATCC TTGTTCTAT GAAC TTGGTC GTCACC

36

(2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CATGAAGCTT ATCCTGGATT TTTCCAAGTA AATCT

35

(2) INFORMATION FOR SEQ ID NO: 293:


- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

GACTGGATCC TTATAAGGGT GAATTAGAAA AAGG

34

(2) INFORMATION FOR SEQ ID NO: 294:

- 
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

GACTAAGCTT CTTATTAGGA TTGTTAGTAG TTG

33

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

GACTGGATCC GAATGTTTCAG GCTCAAGAAA GTTCAGG

37

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GACTAAGCTT TTCCCCTGAT GGAGCAAAGT AATACC

36

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

GACTGGATCC CTTGGGTGTA ACCCATATCC AGCTCCTTCC

40

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

GACTGTCGAC TTCAGCTTGT TTATCTGGGG TTGC

34

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

GACTGGATCC TAGTGATGGT ACTTGCAAG GAAAACAG

38

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

ACTGCTGCAG ATCTTTGCCA CCTAGCTTCT CATTG

35

## (2) INFORMATION FOR SEQ ID NO: 301:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

GTCAGGATCC TGGGATTCAA TATGTCAGAG ATGATACTAG

40

## (2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

CTAGAAGCTT ACGCACCCAT TCACCATTAT CATTG

35

## (2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

GTCAGGATCC GGATAATAGA GAAGCATTA AAACC

35

## (2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AGTCAAGCTT GACAAAATCT TGAAACTCCT CTGGTC

36

## (2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GTCAGGATCC AGATTTTGTGTC GAGGAGTGTGTC ATACC

35

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

AGTCAAGCTT TCCCTTTTTC CCCTTACGAA TCCAGG

36

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GACTGGATCC ATCTGTAGTT TATGCGGATG AAACACTTAT TAC

43

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

GACTGTCGAC GCTTTGGTAG AGATAGAAGT CATG

34

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

GACTGGATCC TTACTTTGGT ATCGTAGATA CAGCCGGC

38

(2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

AGTCAAGCTT TGTTAATTGC GTACCTTCTA AGCGACC

37

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

GACTGGATCC AGCTAAGGTT GCATGGGATG CGATTCCG

37

(2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

GACTGTCGAC CTGGGCTTTA TTAGTTTGAC TAGC

34

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

CAGTGGATCC CTATCACTAT GTAAATAAAG AGA

33

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

ACTGAAGCTT TTCTGTCCCT GTTTGAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

CAGTGGATCC TGAGACTCCT CAATCAATAA CAAA

34

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

ACGTAAGCTT ATAATCAGTA GGAGAACTG AACT

34

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CAGTGGATCC GGATGCTCAA GAAACTGCGG

30

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

GACTAAGCTT TTGCCTCTCA TTCTTGCTTC C

31

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

CAGTGGATCC CGACAAAGGT GAGACTGAG

29

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

ACGTAAGCTT ATTTCTTAAT TCAAGTGTTT TCTCTG

36

(2) INFORMATION FOR SEQ ID NO: 321:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GACTGGATCC AAATCAATTG GTAGCACAAG ATCC

34

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CAGTGTCGAC ATTAGGAGCC ACTGGTCTC

29

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

CAGTGGATCC CAAACAGTCA GCTTCAGGAA C

31

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

GACTCTGCAG TTTAATCTTG TCCCAGGTGG

30

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

GACTGGATCC ATTCGATGAT GCGGATGAAA AG

32

(2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

GACTAAGCTT CATTTGTCTT TGGGTATTTT GCA

33

(2) INFORMATION FOR SEQ ID NO: 327:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

CAGTGGATCC GGAGAGTCGA TCAAAAGTAG

30

(2) INFORMATION FOR SEQ ID NO: 328:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

GTCAGTGCAG TTGCTCGTCT CGAGGTTC

28

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

CAGTGGATCC ATGGACAACA GGAAACTGGG AC

32

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

CAGTAAGCTT ATTAGCTTCT GTACCTGTGT TTG

33

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

GACTGGATCC CGATGGGCTC AATCCAACCC CAGGTCAAGT C

41

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GACTCTGCAG CATAGCTTTA TCCTCTGACA TCATCGTATC

40



(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

GACTGGATCC TTCCAATCAA AAACAGGCAG ATGG

34

(2) INFORMATION FOR SEQ ID NO: 334:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

GACTAAGCTT GAGTCCCATA GTCCAAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 335:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

AGTCGGATCC TATCACAGGA TCGAACGGTA AGACAACC

38

(2) INFORMATION FOR SEQ ID NO: 336:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

ACTGGTCGAC TTCTTTTAAC TCCGCTACTG TGTC

34

(2) INFORMATION FOR SEQ ID NO: 337:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CAGTGGATCC AAGTTCATCG AAGATGGTTG GGAAGTCC

38

(2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

GATCGTCGAC CCGCTCCAC ATGCTCAACC TT

32

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

TGACGGATCC ATCGCTAGCT AGTGAAATGC AAGAAAG

37

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

TGACAAGCTT ATTCGTTTTT GAACTAGTTG CTTTCGT

37

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GACTGGATCC GCACCAGATG GGGCACAAGG TTCAGGG

37

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

TGACAAGCTT AACTTGTAAC GAACAGTTCA ATCTG

35

(2) INFORMATION FOR SEQ ID NO: 343:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

GACTAGATCT TTTTAACCCA ACTGTTGGTA CTTTCC

36

(2) INFORMATION FOR SEQ ID NO: 344:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TGACAAGCTT GTTAGGTGTT ACATTTTGAC CGTC

34

(2) INFORMATION FOR SEQ ID NO: 345:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

ACTGAGATCT TTTTAACCCA ACTGTTGGTA CTTTC

35

(2) INFORMATION FOR SEQ ID NO: 346:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

GACTAAGCTT TCTACGATAA CGATCATTTT CTTTACC

37

(2) INFORMATION FOR SEQ ID NO: 347:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

GACTGTCGAC TCGTAGATAT TTAAGTCTAA GTGAAGCG

38

(2) INFORMATION FOR SEQ ID NO: 348:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

AGTCAAGCTT GTTAGGTGTT ACATTTTGCA AGTC

34

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GACTGGATCC CTTTGTTTTT GAAGGAAGTA AG

32

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

TGACCTGCAG ACGATTTTTG AAAAATGGAG GTGTATC

37

(2) INFORMATION FOR SEQ ID NO: 351:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

CAGTGGATCC CTACTACCTC TCGAGAGAAA G

31

(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

ACTGAAGCTT TTCGCTTTTT ACTCGTTTGA CA

32

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CAGTGGATCC TAAGGTCAAA AGTCAGACCG CTAAGAAAGT GC

42

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

CAGTAAGCTT TAGGGTATCC AAATACTGGT TGTTGATG

38

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

TGACAGATCT TGACGGGTCT CAGGATCAGA CTCAGG

36

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

TGACAAGCTT CAAAGACATC CACCTCTTGA CCTTTG

36

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

GACTGGATCC TAGAGGCTTT GCCAAATGGT GGGAAGGG

38

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

GTCAGTCGAC TTGTTGTAAC ACTTTTCGAG GTTTGGTACC

40

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CAGTGGATCC TCAAAAAGAG AAGGAAACT TGG

33

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CAGTCTGCAG TTTCTTCAAC AAACCTTGTT CTTG

34

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

CAGTGGATCC ACGTTCTATT GAGGACCACT T

31

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

CAGTAAGCTT TTCCTTCTCA GTCAATTCTT TTCC

34

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GACTGGATCC CGCTCAAAAT ACCAGAGGTG TTCAG

35

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

GACTAAGCTT AGTACCATGG GTGTGACAGG TTTGAA

36

## (2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

CTGAGGATCC AATTGTACAA TTAGAAAAAG ATAGC

35

## (2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

TGACAAGCTT GCGTTGACTA GGTTC TGCAA TGCC

34

## (2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

GACTGGATCC TCTGACCAAG CAAAAAGAAG CAGTCAATGA

40

## (2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

TCAGCAGCTG ATCATTGACT TTACGATTTG CTCC

34

## (2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 41 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

GACTGGATCC GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC G

41

(2) INFORMATION FOR SEQ ID NO: 370:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAGAAGCTT ATTTTTTGTT TCCTTAATGC GTT

33

(2) INFORMATION FOR SEQ ID NO: 371:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

GACTGGATCC GGGACAAATT CAAAAAATA GGCAAGAGG

39

(2) INFORMATION FOR SEQ ID NO: 372:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

GTCAAAGCTT TGGCTCTTTG ATTGCCAACA ACTG

34

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

GACTGGATCC TCGCTACCAG CAACAAAGCG AGCAAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

GACTAAGCTT ACTTTTTTCT TTTTCCACAC GA

32

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

CAGTGGATCC GAACCGACAA GTCGCCCACT ATCAAGACT

39

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CTGAAAGCTT TGAATTCTCT TTCTTTTCAG GCT

33

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

TCGAGGATCC GGTGTGTCGGC TGGCAATATA TCCCGT

36

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CAGTAAGCTT CCGAACCCAT TCGCCATTAT AGTTGAC

37

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

AGTCGGATCC GGCCAAATCA GAATGGGTAG AAGAC

35

(2) INFORMATION FOR SEQ ID NO: 380:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

TGACCTGCAG CTTCTCATTG ATTTTCATCA TCAC

34

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACTGGATCC ATTTGCAGAT GATTCTGAAG GATGG

35

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

TCAGCTGCAG CTTAACCCAT TCACCATTCT AGTTTAAG

38

(2) INFORMATION FOR SEQ ID NO: 383:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

GACTGGATCC TGTCGCTGCA AATGAACTG AAGTAGC

37

(2) INFORMATION FOR SEQ ID NO: 384:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

GACTAAGCTT ATACCAAACG CTGACATCTA CGCG

34

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

AGTCAGATCT TACGTCTCAG CCTACTTTTG TAAGAGC

37

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

GACTAAGCTT AACCCATTCA CCATTGGCAT TGAC

34

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

CAGTGGATCC TGGACAGGTG AAAGGTCATG CTACATTTGT G

41

(2) INFORMATION FOR SEQ ID NO: 388:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

GACTAAGCTT CAACCATTGA GACCTTGCAA CAC

33

(2) INFORMATION FOR SEQ ID NO: 389:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

GTCAGGATCC GATTGCTCCT TTGAAGGATT TGAGAGAAAC C

41

(2) INFORMATION FOR SEQ ID NO: 390:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GACTAAGCTT CGATCAAAGA TAAGATAAAT ATATATAAAG T

41

(2) INFORMATION FOR SEQ ID NO: 391:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GACTGGATCC TAGGTCATAT GGGACTTTTTT TTCTACAACA AAATAGG

47

(2) INFORMATION FOR SEQ ID NO: 392:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

TGACAAGCTT ATCTATCAGC TCATTTAATC GTTTTTG

37

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CTGAGGATCC CAACGTTGAG AATTATTTGC GAATG

35

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

TGACAAGCTT GAGTCTACAA AAGTAATGTA C

31

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

GTCAGGATCC CTACTATCAA TCAAGTTCTT CAGCC

35

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

TGACAAGCTT GACTGAGGCT TGGACCAGAT TGAAAAG

37

## (2) INFORMATION FOR SEQ ID NO: 397:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

GACTGGATCC GACAAAAACA TTAAACGTC CTGAGG

36

## (2) INFORMATION FOR SEQ ID NO: 398:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

GACTAAGCTT AGCACGAACT GTGACGCTGG TTCC

34

## (2) INFORMATION FOR SEQ ID NO: 399:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

GACTGGATCC TTCTCAGGAG ACCTTTAAAA ATATC

35

## (2) INFORMATION FOR SEQ ID NO: 400:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

GACTAAGCTT GTTGCCATC TTGTACATAC C

31

## (2) INFORMATION FOR SEQ ID NO: 401:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

GACTGGATCC AGTAAATGCG CAATCAAATT C

31

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

AGTCCTGCAG GTATTTAGCC CAATAATCTA TAAAGCT

37

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

CAGTGGATCC TTACCGCGTT CATCAAGATG TC

32

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

GACTAAGCTT GCCAGATGTT GAAAAGAGAG TG

32

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

GACTGGATCC GTGGATGGGC TTAACTATC TTCGTATTCG

40

(2) INFORMATION FOR SEQ ID NO: 406:



- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

AGTCAAGCTT GCTAGTCTTC ACTTTCCCTT TCC

33

(2) INFORMATION FOR SEQ ID NO: 407:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

GACTGTCGAC ACTAAACCAG CATCGTTCGC AGGA

34

(2) INFORMATION FOR SEQ ID NO: 408:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

CTGACTGCAG CTTCTTGAAG AAATAATGAT TGTGG

35

(2) INFORMATION FOR SEQ ID NO: 409:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

CAGTGGATCC TGACTACCTT GAAATCCCAC TT

32

(2) INFORMATION FOR SEQ ID NO: 410:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

CAGTAAGCTT TTTTAAAGG TTGTAGAATG ATTTCAATC

39

(2) INFORMATION FOR SEQ ID NO: 411:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

CAGTGTCGAC TCGTATCTTT TTTTGGAGCA ATGTT

35

(2) INFORMATION FOR SEQ ID NO: 412:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

GACTAAGCTT AAATGTTCCG ATACGGGTGA TTG

33

(2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

CAGTGGATCC GGACTCTCTC AAAGATGTGA AAG

33

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

GACTAAGCTT CTTGAGTTTG TCAAGGATTG CTTT

34

(2) INFORMATION FOR SEQ ID NO: 415:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

CAGTGGATCC CAAGAAATCC TATCATCTCT TCCAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 416:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GACTAAGCTT TTCAGAACTA AAAGCCGCAG CTT

33

(2) INFORMATION FOR SEQ ID NO: 417:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

GACTGGATCC ACGAAATGCA GGCAGACAG

30

(2) INFORMATION FOR SEQ ID NO: 418:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

CAGTAAGCTT ATCAACATAA TCTAGTAAAT AAGCGT

36

(2) INFORMATION FOR SEQ ID NO: 419:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

CAGTGGATCC TGTATAGTTT TTAGCGCTTG TTCTTC

36

(2) INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

GTCAAAGCTT TGATAGAGTG TCATAATCTT CTTTAG

36

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

GACTGGATCC GTGTGTCGAG CATATTCTGA AG

32

(2) INFORMATION FOR SEQ ID NO: 422:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

CAGTAAGCTT ACTTTTACCA TTTCTTTGTT CTGCATC

37

(2) INFORMATION FOR SEQ ID NO: 423:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

GACTGTCGAC GTGTTTGGAT AGCATTGAGA ATCAGACG

38

(2) INFORMATION FOR SEQ ID NO: 424:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

CAGTAAGCTT CGGAAGTAAA GACAATTTTT CC

32

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

CAGTGGATCC GTGCCTAGAT AGTATTATTA CTCAAAC

37

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

GACTAAGCTT TTTGCTTATT TCTCTCAATT TTTC

34

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

CAGTGGATCC CATTGAGAAG CAGACCTATC AAAATC

36

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

ACTGAAGCTT ATGTAATTTT TTAGATTTT CAATATTTT CAG

43

## (2) INFORMATION FOR SEQ ID NO: 429:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AGTCGGATCC TAAGGCTGAT AATCGTGTTT AAATG

35

## (2) INFORMATION FOR SEQ ID NO: 430:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

GACTAAGCTT AAAATTAGAT AGACGTTGAG T

31

## (2) INFORMATION FOR SEQ ID NO: 431:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

AGTCGGATCC CTGTGGCAAT CAGTCAGCTG CTTCC

35

## (2) INFORMATION FOR SEQ ID NO: 432:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

GACTGTCGAC TTTAATCTTG TCCCAGGTGG TTAATTTGCC

40

## (2) INFORMATION FOR SEQ ID NO: 433:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

ACTGGTCGAC TTGTCAACAA CAACATGCTA CTTCTGAG

38

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

GACTCTGCAG AAGTTTAACC CACTTATCAT TATCC

35

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

ACTGGGATCC TTGTTTCAGGC AAGTCCGTGA CTAGTGAAC

39

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

GACTAAGCTT GGCTAATTCC TTCAAAGTTT GCA

33

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

AGTCGGATCC CTCGCAAATT GAAAAGGCGG CAGTTAGCC

39

(2) INFORMATION FOR SEQ ID NO: 438:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

GACTAAGCTT GTAAATAAGC GTACCTTTTT CTTC

35

(2) INFORMATION FOR SEQ ID NO: 439:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

TCAGGGATCC TTGTCACTCA GGTCTAATG GTTCTCAG

38

(2) INFORMATION FOR SEQ ID NO: 440:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

AGTCAAGCTT GGCATTGGCG TCGCCGTCCT TC

32

(2) INFORMATION FOR SEQ ID NO: 441:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

GACTGGATCC GGAACTTCA CAGGATTTTA AAGAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 442:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

GACTGTCGAC AATCAATCCT TCTTCTGCAC TTCT

34

(2) INFORMATION FOR SEQ ID NO: 443:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

CAGTGGATCC TGTGGTCGAA GTTGAGACTC CTCAATC

37

(2) INFORMATION FOR SEQ ID NO: 444:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

GACTAAGCTT TTCTTCAAAT TTATTATCAG C

31

(2) INFORMATION FOR SEQ ID NO: 445:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

AGTCGGATCC AACACCTGTA TATAAAGTTA CAGCAATCG

39

(2) INFORMATION FOR SEQ ID NO: 446:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

GACTGTCGAC TACTTGACCG AATGCGTCGA ATGTACG

37

(2) INFORMATION FOR SEQ ID NO: 447:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

CTGAGGATCC ATTAGACAGA TTAATTGAAA TCGG

34

(2) INFORMATION FOR SEQ ID NO: 448:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

GACTGTGCGAC TTAAAGATT GAAGTTTAA AGCT

34

(2) INFORMATION FOR SEQ ID NO: 449:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

TGACGGATCC TAAGACAGAT GAACGGAGCA AGGTG

35

(2) INFORMATION FOR SEQ ID NO: 450:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

CTGAAAGCTT TAAGGCTTCC TCAATGAGTT TGTCT

35

(2) INFORMATION FOR SEQ ID NO: 451:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

GACTGGATCC CTGTGAGAAT CAAGCTACAC CCA

33

(2) INFORMATION FOR SEQ ID NO: 452:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

CTGAAAGCTT TTGTAAGTGA GATTGATCTG GGAG

34

(2) INFORMATION FOR SEQ ID NO:453:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Leu Ala Ser Gly Ala Cys  
1 5

(2) INFORMATION FOR SEQ ID NO:454:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Leu Pro Xaa Thr Gly Xaa  
1 5